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A METHOD FOR PRODUCING INFLUENZA HEMAGGLUTININ MULTIVALENT VACCINES

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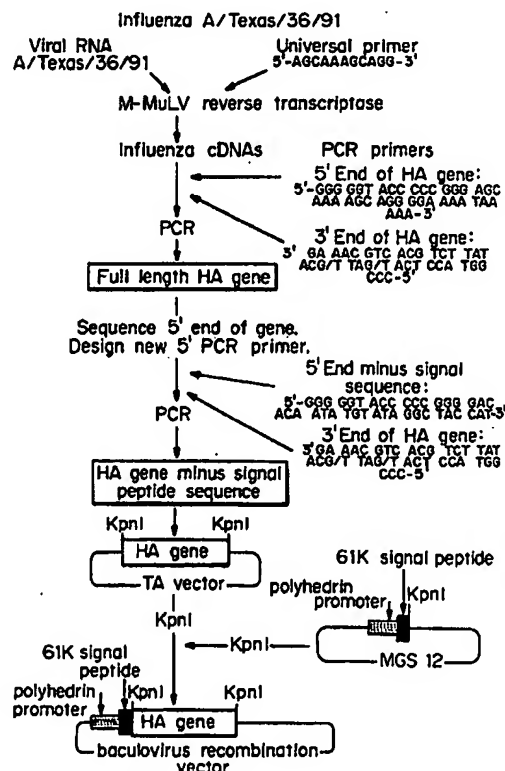
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A method of preparing a recombinant influenza vaccine using DNA technology is provided. The resulting vaccine is a multivalent, preferably trivalent, influenza vaccine based on a mixture of recombinant hemagglutinin antigens cloned from influenza viruses having epidemic potential. The recombinant hemagglutinin antigens are full length, uncleaved (HAO), glycoproteins produced from baculovirus expression vectors in cultured insect cells and purified under non-denaturing conditions. In the preferred embodiment, the cloned HA genes are then modified by deletion of the natural hydrophobic signal peptide sequences and replacing them with a new baculovirus chitinase signal peptide. A general approach for the efficient extraction and purification of recombinant HA protein produced in insect cells is also disclosed for the purification of rHA proteins from A sub-types and B type influenza viruses.



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**A METHOD FOR PRODUCING INFLUENZA
HEMAGGLUTININ MULTIVALENT VACCINES**

Background of the Invention

5 The present invention is generally in the area
of recombinant influenza vaccines.

 Epidemic influenza occurs annually and is a
cause of significant morbidity and mortality
worldwide. Children have the highest attack rate,
10 and are largely responsible for transmission of
influenza viruses in the community. The elderly
and persons with underlying health problems are at
increased risk for complications and
hospitalization from influenza infection. In the
15 United States alone, more than 10,000 deaths
occurred during each of seven influenza seasons
between 1956 and 1988 due to pneumonia and
influenza, and greater than 40,000 deaths were
reported for each of two seasons (Update: Influenza
20 Activity - United States and Worldwide, and
Composition of the 1992-1993 Influenza Vaccine,
Morbidity and Mortality Weekly Report. U.S.
Department of Health and Human Services, Public
Health Service, 41/No. 18:315-323, 1992.)
25 Influenza viruses are highly pleomorphic particles
composed of two surface glycoproteins,
hemagglutinin (HA) and neuraminidase (NA). The HA
mediates attachment of the virus to the host cell
and viral-cell membrane fusion during penetration
30 of the virus into the cell. The influenza virus
genome consists of eight single-stranded negative-
sense RNA segments of which the fourth largest
segment encodes the HA gene. The influenza viruses

are divided into types A, B and C based on antigenic differences. Influenza A viruses are described by a nomenclature which includes the sub-type or type, geographic origin, strain number, and year of isolation, for example, A/Beijing/353/89. There are at least 13 sub-types of HA (H1-H13) and nine subtypes of NA (N1-N9). All subtypes are found in birds, but only H1-H3 and N1-N2 are found in humans, swine and horses (Murphy and Webster, "Orthomyxoviruses", in *Virology*, ed. Fields, B.N., Knipe, D.M., Chanock, R.M., 1091-1152 (Raven Press, New York, (1990)).

Antibodies to HA neutralize the virus and form the basis for natural immunity to infection by influenza (Clements, "Influenza Vaccines", in *Vaccines: New Approaches to Immunological Problems*, ed. Ronald W. Ellis, pp. 129-150 (Butterworth-Heinemann, Stoneham, MA 1992)). Antigenic variation in the HA molecule is responsible for frequent outbreaks to influenza and for limited control of infection by immunization.

The three-dimensional structure of HA and the interaction with its cellular receptor, sialic acid, has been extensively studied (Wilson, et al, "Structure of the hemagglutinin membrane glycoprotein of influenza virus at 3A' resolution" *Nature* 289:366-378 (1981); Weis, et al, "Structure of the influenza virus hemagglutinin complexed with its receptor, sialic acid" *Nature*, 333:426-431 (1988); Murphy and Webster, 1990). The HA molecule is present in the virion as a trimer. Each monomer exists as two chains, HA1 and HA2, linked by a single disulfide bond. Infected host cells produce a precursor glycosylated polypeptide (HA0) with a molecular weight of about 85,000, which is subsequently cleaved into HA1 and HA2.

The presence of influenza HA-specific neutralizing IgG and IgA antibody is associated with resistance to infection and illness (Clements, 1992). Inactivated whole virus or partially purified (split subunit) influenza vaccines are standardized to the quantity of HA from each strain. Influenza vaccines usually include 7 to 25 micrograms HA from each of three strains of influenza.

10 The role of the other major surface glycoprotein, NA, in protective immunity of antibody or T-cell responses against influenza has not been defined. Neuraminidase is very labile to the process of purification and storage (Murphy and
15 Webster, 1990) and the quantity of NA in the current influenza vaccines is not standardized. Purified HA but not NA vaccine prevents disease in animals challenged with influenza (Johansson, et al, "Purified influenza virus hemagglutinin and
20 neuraminidase are equivalent in stimulation of antibody response but induce contrasting types of immunity to infection" J. Virology, 63:1239-1246 (1989)). An experimental vaccine based on neuraminidase antigen was not found to be
25 protective in a human trial (Orga et al, J. Infect. Dis. 135:499-506 (1977)).

Licensed influenza vaccines consist of formalin-inactivated whole or chemically split subunit preparations from two influenza A subtype
30 (H1N1 and H3N2) and one influenza B subtype viruses. Prior to each influenza season, the U.S. Food and Drug Administration's Vaccines and Related Biologicals Advisory Committee recommends the composition of a trivalent influenza vaccine for
35 the upcoming season. The 1992-93 vaccine contained A/Texas/36/91-like(H1N1), A/Beijing/353/89-

like(H3N2), and B/Panama/45/90 viruses. The FDA has advised that the 1993-94 influenza vaccine should contain the same Texas and Panama strains and a new influenza A Beijing strain

5 (A/Beijing/32/92).

Vaccination of high-risk persons each year before the influenza season is the most effective measure for reducing the impact of influenza.

10 Limitations of the currently available vaccines include low use rates; poor efficacy in the elderly and in young children; production in eggs; antigenic variation; and adverse reactions.

The Center for Disease Control (CDC) estimates that less than 30% of the individuals at high-risk
15 for influenza are vaccinated each year (MMWR, 1992). The current inactivated vaccines achieve a high rate of protection against disease among normal healthy adults when the antigens of the vaccine and those of the circulating influenza
20 viruses are closely related. Among the elderly, the rate of protection against illness is much lower, especially for those who are institutionalized (Clements, 1992). In a recent study by Powers and Belshe, J. Inf. Dis. 167:584-
25 592 (1993), significant antibody responses to a trivalent subvirion influenza vaccine were observed in less than 30 percent of subjects 65 years old or older.

Seed viruses for influenza A and B vaccines
30 are naturally occurring strains that replicate to high titers in the allantoic cavity of chicken eggs. Alternatively, the strain for the influenza A component is a reassortant virus with the correct surface antigen genes. A reassortant virus is one
35 that, due to segmentation of the viral genome, has characteristics of each parental strain. When more

than one influenza viral strains infect a cell, these viral segments mix to create progeny virion containing various assortments of genes from both parents.

5 Protection with current whole or split influenza vaccines is short-lived and wanes as antigenic drift occurs in epidemic strains of influenza. Influenza viruses undergo antigenic drift as a result of immune selection of viruses
10 with amino acid sequence changes in the hemagglutinin molecule. Ideally, the vaccine strains match the influenza virus strains causing disease. The current manufacturing process for influenza vaccines, however, is limited by
15 propagation of the virus in embryonated chicken eggs. Not all influenza virus strains replicate well in eggs; thus the viruses must be adapted or viral reassortants constructed. Extensive heterogeneity occurs in the hemagglutinin of egg-
20 grown influenza viruses as compared to primary isolates from infected individuals grown in mammalian cells (Wang, et al, Virology 171:275-279 (1989); Rajakumar, et al, Proc. Natl. Acad. Sci. USA 87:4154-4158 (1990)). The changes in HA during
25 the selection and manufacture of influenza vaccines can result in a mixture of antigenically distinct subpopulations of virus. The viruses in the vaccine may therefore differ from the variants within the epidemic strains, resulting in
30 suboptimal levels of protection.

Immediate hypersensitivity reactions can occur in persons with severe egg allergy due to residual egg protein in the vaccine. The 1976 swine influenza vaccine was associated with an increased
35 frequency of Guillain-Barré syndrome. Subsequent vaccines prepared from other influenza strains

have, thus far, not been observed to increase the occurrence of this rare disease.

A method of producing an influenza vaccine that does not require propagation in eggs would
5 result in a purer product that would be less likely to cause an adverse immune reaction. In addition, a purer vaccine preparation would not require virus inactivation or organic extraction of viral
10 membrane components, thereby avoiding denaturation of antigenic epitopes and safety concerns due to residual chemicals in the vaccine.

In addition, an influenza vaccine produced in the absence of egg propagation would avoid the genetic heterogeneity that occurs during adaptation
15 and passage through eggs. This would result in a vaccine that is better matched with influenza epidemic strains, resulting in improved efficacy.

It is therefore an object of the present invention to provide a method of producing an
20 influenza vaccine that does not require replication in eggs.

It is a further object of the present invention to provide a method of producing an influenza vaccine that is rapid and cost-efficient,
25 highly purified and allows production of vaccines from primary sources of influenza.

Summary of the Invention

A method of preparing a recombinant influenza hemagglutinin protein by expression in insect cells using a baculovirus expression system is provided. The resulting protein is useful in making a multivalent influenza vaccine based on a mixture of recombinant hemagglutinin antigens cloned from influenza viruses having epidemic potential. The recombinant hemagglutinin proteins are full length, uncleaved (HA0) glycoproteins including both the HA1 and HA2 subunits (HA0) purified under non-denaturing conditions to 95% or greater purity, preferably 99% purity.

A process for cloning influenza hemagglutinin genes from influenza A and B viruses using specially designed oligonucleotide probes and polymerase chain reaction (PCR) methodology is also disclosed. In the preferred embodiment, the cloned HA genes are modified by deletion of the nucleotides encoding the natural hydrophobic signal peptide sequences and replacement with a new baculovirus signal peptide, to yield a sequence encoding the signal peptide immediately abutting the hemagglutinin. These chimeric genes are introduced into baculovirus expression vectors so that the baculovirus polyhedrin promoter directs the expression of recombinant HA proteins in infected insect cells. The 18 amino acid baculovirus signal peptide directs the translation of rHA into the insect cell glycosylation pathway and is not present on the mature rHA glycoprotein. In the preferred embodiment, a vector is designed that does not encode any intervening amino acids between the signal peptide and hemagglutinin protein.

This methodology can be extended to all types of influenza viruses, including but not limited to the prevalent A (H1N1) sub-type, the A(H3N2) sub-type, and the B type that infect humans, as well as the influenza viruses which infect other mammalian and avian species.

A general approach for the efficient extraction and purification of recombinant HA protein produced in insect cells is disclosed for the purification of rHA proteins from A sub-types and B type influenza viruses. The recombinant vaccine can be developed from primary sources of influenza, for example, nasal secretions from infected individuals, rather than from virus adapted to and cultured in chicken eggs. This allows rapid development of vaccine directly from epidemic strains of influenza and avoids the problems arising from adaptation of the virus for culture in eggs, as well as patient reaction to egg contamination in the resulting vaccine.

Examples demonstrate the formulation and clinical efficacy of vaccine in an immunizing dosage form including purified rHA antigens from three strains of influenza virus recommended by the FDA for the 1993/1994 and 1994/1995 influenza epidemic seasons. Functional immunity was measured using assays that quantitate antibodies that bind to influenza hemagglutinin, that block the ability of influenza virus to agglutinate red blood cells, or that neutralize the influenza virus. Protective immune responses with rHA vaccines were measured in animals that are susceptible to influenza infection or in human challenge studies.

Brief Description of the Drawings

Figure 1 is a schematic of the cloning of HA genes from influenza A strains from purified viral RNA preparations, purification of expressed rHA, and biological characterization of rHA.

Abbreviations: FDA, Food and Drug Administration; MDCK, Madin Darby Canine Kidney; TPCK, tosylphenylalanyl chloromethylketone; RNA, ribonucleic acid; cDNA, complementary deoxyribonucleic acid; HA, hemagglutinin; FBS, Fetal Bovine Serum; PCR, Polymerase Chain Reaction; and BV, Baculovirus.

Figure 2 is a more detailed schematic of the method of Figure 1 applied to the cloning and expression of the HA gene of the Influenza A/Texas/36/91 strain. Influenza HA gene was obtained from RNA purified from MDCK cells infected with influenza A/Texas/36/91 using reverse transcriptase and universal primer (SEQ ID NO. 1) followed by two rounds of PCR amplification and cloning. As shown, in the first round of PCR reactions, 5' end primer SEQ ID NO. 2 and 3' end primer SEQ ID NO. 3 were used. In the second round of PCR reactions, 5' end primer SEQ ID NO. 4 and 3' end primer SEQ ID NO. 5 were used. A baculovirus recombination vector was constructed containing the polyhedrin promoter and a signal peptide sequence from the baculovirus 61K gene (a baculovirus gene that encodes a signal peptide having a molecular weight of approximately 61,000), followed by the complete coding sequences for the mature HA protein. This recombination vector was then used to make a baculovirus expression vector that produces HA from this strain of the virus.

9 a

Figure 3 is a graph of the anti-HA immune response in mice, day 42, n=5, graphing antibody titer for rHA0-neat; Fluzone® vaccine, and rHA0-alum, at dosages of 0.5 μ g (dark bars), 0.1 μ g (shaded bars), 0.02 μ g (dotted bars), and 0.004 μ g (open bars).

Figures 4a, 4b, and 4c are graphs of the anti-HA immune response in mice immunized with rHA or licensed trivalent vaccine, 1994-1995 formula, weeks post vaccination versus HIA titer, for HAI A/Texas/36/91 (Figure 4a), HAI A/Shangdong/9/93 (Figure 4b), and HAI B/Panama/45/90 (Figure 4c), rHA (diamonds) and FLUVIRON® attenuated vaccine cultured in eggs (squares).

10 Detailed Description of the Invention

A method of preparing a recombinant influenza vaccine is described. A full length, uncleaved (HA0), hemagglutinin antigen from an influenza virus is produced with baculovirus expression vectors in cultured insect cells and purified under non-denaturing conditions. Two or more purified hemagglutinin antigens from influenza A and/or influenza B strains are mixed together to produce a multivalent influenza vaccine. The recombinant antigens may be combined with an adjuvant carrier for increased efficacy.

The use of recombinant DNA technology to produce influenza vaccines offers several advantages: a recombinant DNA influenza vaccine can be produced under safer and more stringently controlled conditions; propagation with infectious influenza in eggs is not required; recombinant HA protein can be more highly purified, virtually eliminating side effects due to contaminating proteins; purification procedures for recombinant HA do not have to include virus inactivation or organic extraction of viral membrane components, therefore avoiding denaturation of antigens and additional safety concerns due to residual chemicals in the vaccine; production of HA via

recombinant DNA technology provides an opportunity to avoid the genetic heterogeneity which occurs during adaptation and passage through eggs, which should make it possible to better match vaccine stains with influenza epidemic stains, resulting in improved efficacy; and a recombinant approach may also allow for strain selection later in the year, thereby allowing time for selections based on more reliable epidemiological data.

10 Baculovirus Expression System.

Baculoviruses are DNA viruses in the family *Baculoviridae*. These viruses are known to have a narrow host-range that is limited primarily to Lepidopteran species of insects (butterflies and moths). The baculovirus *Autographa californica* Nuclear Polyhedrosis Virus (AcNPV), which has become the prototype baculovirus, replicates efficiently in susceptible cultured insect cells. AcNPV has a double-stranded closed circular DNA genome of about 130,000 base-pairs and is well characterized with regard to host range, molecular biology, and genetics.

Many baculoviruses, including AcNPV, form large protein crystalline occlusions within the nucleus of infected cells. A single polypeptide, referred to as a polyhedrin, accounts for approximately 95% of the protein mass of these occlusion bodies. The gene for polyhedrin is present as a single copy in the AcNPV viral genome. Because the polyhedrin gene is not essential for virus replication in cultured cells, it can be readily modified to express foreign genes. The foreign gene sequence is inserted into the AcNPV gene just 3' to the polyhedrin promoter sequence such that it is under the transcriptional control of the polyhedrin promoter.

Recombinant baculoviruses that express foreign genes are constructed by way of homologous recombination between baculovirus DNA and chimeric plasmids containing the gene sequence of interest.

- 5 Recombinant viruses can be detected by virtue of their distinct plaque morphology and plaque-purified to homogeneity.

Baculoviruses are particularly well-suited for use as eukaryotic cloning and expression vectors.

- 10 They are generally safe by virtue of their narrow host range which is restricted to arthropods. The U.S. Environmental Protection Agency (EPA) has approved the use of three baculovirus species for the control of insect pests. AcNPV has been
15 applied to crops for many years under EPA Experimental Use Permits.

- AcNPV wild type and recombinant viruses replicate in a variety of insect cells, including continuous cell lines derived from the fall
20 armyworm, *Spodoptera frugiperda* (Lepidoptera; Noctuidae). *S. frugiperda* cells have a population doubling time of 18 to 24 hours and can be propagated in monolayer or in free suspension cultures.

- 25 Recombinant HA proteins can be produced in, but not limited to, cells derived from the Lepidopteran species *Spodoptera frugiperda*. Other insect cells that can be infected by baculovirus, such as those from the species *Bombix mori*,
30 *Galleria mellonella*, *Trichoplusia ni*, or *Lamprolaima dispar*, could also be used as a suitable substrate to produce recombinant HA proteins.

- The most preferred host cell line for protein production from recombinant baculoviruses is
35 Sf900+. Another preferred host cell line for protein production from recombinant baculoviruses

is Sf9. Sf900+ and Sf9 are non-transformed, non-tumorigenic continuous cell lines derived from the fall armyworm, *Spodoptera frugiperda* (Lepidoptera; Noctuidae). Sf900+ and Sf9 cells are propagated at
5 28±2°C without carbon dioxide supplementation. The culture medium used for Sf9 cells is TNMFH, a simple mixture of salts, vitamins, sugars and amino acids, supplemented with 10% fetal bovine serum. Aside from fetal bovine serum, no other animal
10 derived products (i.e, trypsin, etc.) are used in cell propagation. Serum free culture medium (available as Sf900 culture media, Gibco BRL, Gaithersburg, MD) can also be used to grow Sf9 cells and is preferred for propagation of Sf900+
15 cells.

Sf9 cells have a population doubling time of 18-24 hours and can be propagated in monolayer or in free suspension cultures. *S. frugiperda* cells have not been reported to support the replication
20 of any known mammalian viruses.

It will be understood by those skilled in the art that the expression vector is not limited to a baculovirus expression system. The recombinant HA proteins can also be expressed in
25 other expression vectors such as Entomopox viruses (the poxviruses of insects), cytoplasmic polyhedrosis viruses (CPV), and transformation of insect cells with the recombinant HA gene or genes constitutive expression.

30 Isolation of Influenza strains.

One or more influenza strains are isolated from individuals infected with the disease. Preferably, the influenza strains are those identified by the Food and Drug Administration
35 (FDA) or CDC to have epidemic potential for the subsequent influenza season. An advantage of the

method described herein is that clinical samples, such as nasal secretions, from patients infected with influenza can be used as a direct source of virus. Alternatively, they can be obtained from
5 the FDA or CDC.

Propagation of Influenza strains.

The strains are then propagated in cells producing high viral titers, such as Madin Darby Canine Kidney (MDCK) cells (available from the
10 American Type Culture Collection under accession number ATCC CCL34). For example, MDCK cells are infected in the presence of tosylphenylalanyl chloromethylketone (TPCK) partially inactivated trypsin and fetal bovine serum concentrations
15 optimized to produce the highest titers of first passage virus. The MDCK cells are infected with the influenza strains at a low multiplicity of infection (0.1 to 0.5) as determined by a standard HA assay (Rosen, "Hemagglutination with Animal
20 Viruses" in *Fundamental Techniques in Virology*, ed. K. Habel and N.P. Salzman, pp. 276-28 (Academic Press, New York 1969), the teachings of which are incorporated herein). The infected cells are incubated at 33°C for 48 hours, and the media
25 assayed for virus production using the hemagglutination activity assay. The conditions yielding the highest HA activity are then used to prepare large stocks of influenza virus.

Purification of Virus.

30 Viral particles produced from the first passage are purified from the media using a known purification method such as sucrose density gradient centrifugation. For example, virus is harvested 24-48 hours post infection by
35 centrifuging media of influenza infected MDCK cells. The resulting viral pellet is resuspended

in buffer and centrifuged through a buffered sucrose gradient. The influenza virus band is harvested from the 40-45% sucrose region of the gradient, diluted with buffer and pelleted by centrifugation at 100,000 x g. The purified virus pellet is resuspended in buffer and stored at -70°C.

Cloning of Influenza Hemagglutinin Genes.

An overview of the methods for cloning HA genes is provided in Figure 1. Basically, cells are infected with the influenza strain to be cloned. Virus is harvested from the cell media and either viral RNA, for Influenza A strains, or mRNA, for Influenza B strains, is isolated. Viral RNA (-RNA) is extracted from purified virions and analyzed on formaldehyde agarose gels using standard procedures. cDNA is synthesized, using either an universal primer system for the viral RNA from the Influenza A strains or random primers for the mRNA from Influenza B strains. Plus-standard complimentary DNA (cDNA) is made using a universal oligonucleotide primer (5'-AGCAAAAGCAGG-3' (SEQ ID NO. 1)) which is homologous to all hemagglutinin RNA segments in influenza A and B viruses (Davis et al, "Construction and characterization of a bacterial clone containing the hemagglutinin gene of the WSN strain (HON1) of influenza virus" Gene, 10:205-218 (1980)). Primers are designed that are homologous to conserved regions at the 5' and 3' end of influenza hemagglutinin genes. Both 5' and 3' primers also have restriction enzyme sites at the ends that are not found within the hemagglutinin genes.

The appropriate influenza A or B primers and influenza cDNA are mixed and the hemagglutinin gene segments amplified using standard PCR procedures.

The resulting double-stranded DNA fragments contain entire mature hemagglutinin coding sequences. The polymerase chain reaction ("PCR") is used to amplify the total HA gene, which is then cloned into a suitable bacterial host such as *E. coli*. The 5' ends are sequenced to identify the signal peptide of the HA genes, then PCR is used to amplify the HA genes minus the signal peptide. This is then subcloned into a plasmid transfer vector containing the AcNPV polyhedrin promoter. The resulting transfer vectors contain the following 5'→3' sequences: Polyhedrin promoter from the baculovirus *A. californica* NPV, an ATG translational start codon, a 61K baculovirus signal peptide, the coding sequences for mature hemagglutinin, the natural hemagglutinin translational termination codon, the polyhedrin RNA polyadenylation signal, and flanking baculovirus DNA.

A purified chimeric transfer plasmid DNA containing a cloned hemagglutinin gene is then mixed with AcNPV wild type DNA, co-precipitated with calcium and transfected into *S. frugiperda* cells. Recombinant baculoviruses are selected on the basis of plaque morphology and further purified by additional rounds of plaque-purification. Cloned recombinant baculoviruses are screened for hemagglutinin expression and a single baculovirus expression vector is selected to produce a Master Virus Bank.

Influenza A Strains:

HA genes from influenza A strains are cloned from purified viral RNA preparations. Viral RNA is extracted from 100-200 microliters of purified influenza A virions containing 1,000-2,000 hemagglutination units (HAU) of influenza. One HAU

is the amount of virus that will agglutinate 50% of the red blood cells in the standard agglutination assay (Rosen, 1969). The virions are treated with proteinase K to digest protein, then the viral RNA is extracted with equal volumes of phenol and chloroform, and precipitated with ethanol in the presence of tRNA carrier. The viral RNA is resuspended in buffer and digested with RNase-free DNase to remove any contaminating DNA, then the extraction and precipitation steps repeated. Viral RNA (vRNA) is then analyzed using formaldehyde agarose gels as described by Maniatis, et al. Molecular Cloning: A Laboratory Manual. pp. 86-96 and 366-367 (Cold Spring Harbor Lab., Cold Spring, N.Y. 1982).

Influenza B Strains:

HA genes from influenza B strains are cloned from total messenger RNA (mRNA) extracted from cells infected with the influenza B-strain. Total RNA is then extracted from the infected cells. The harvested cells are lysed in the presence of guanidinium thiocyanate and total cell RNA is purified, using, for example, the RNA Extraction Kit from Pharmacia Biotech Inc. (Piscataway, NJ) Total mRNA is extracted from cellular RNA using Oligo-(dT)-cellulose spun columns, using, for example, the mRNA Purification Kit from Pharmacia Biotech Inc.

Expression and Processing of Recombinant Hemagglutinin in Insect Cells.

Recombinant hemagglutinin antigens are expressed at high levels in *S. frugiperda* cells infected with AcNPV-hemagglutinin vectors. The primary gene product is unprocessed, full length hemagglutinin (rHA0) and is not secreted but remains associated with peripheral membranes of infected cells. This recombinant HA0 is a 68,000

molecular weight protein which is glycosylated with N-linked, high-mannose type glycans distinct from the glycans produced by expression of the viral proteins in mammalian or avian cells. There is evidence that rHA0 forms trimers post-translationally which accumulate in cytoplasmic membranes.

Vectors for Expression of HAO and other Proteins

HAO is a better vaccine due to its superior stability as compared to the HA1/HA2 complex, and maintains correct folding during purification and storage. The superior stability is particularly apparent with the B strains, resulting in titers that are about five fold greater than obtained with commercially available attenuated B strains.

As described below in the examples, when the HA genes were cloned in pMGS12 via restriction sites, the HA mature signal peptide was removed and replaced with the baculovirus chitinase signal peptide, referred to as the 61 kD signal peptide. Since the HA gene is connected to the chitinase signal peptide through a cleavage site, there are between three and five amino acids, depending on the restriction site selected, between the mature HAO protein and the 61 kD signal peptide. Although not a problem with the A strains of influenza, the B strain HAO expressed with the additional amino acids did not fold properly.

Two ways to overcome this problem were developed. The first is to use a new vector, pMGS3, which does not encode the 61 kD signal peptide. HAO with its native signal peptide is cloned into the vector and expressed. When characterized by SDS-PAGE, B strain HAO expressed in this vector shows better glycosylation and

processing than when expressed in pMGS12. The HAO folded so well that it can be quantitatively converted to HA1/HA2. Unfortunately, as determined by Western blotting, the yield is not as high. The
5 second method increases the yield by using the 61 kD signal peptide in pMGS12 to guide expression where the HAO gene was inserted without the use of restriction enzymes. The new vector, including the 61 kD signal peptide and HAO gene, without sequence
10 encoding extraneous intervening amino acids, is referred to as pMGS27.

pMGS27 can be used for cloning and expression of any gene in a baculovirus expression system. The target gene, instead of being cloned into the
15 vector by restriction and ligation, is cloned into the vector by annealing. Reagents are available from Clontech in their PCR-direct Cloning System. pMGS27 was designed so that it can be linearized at the end of the chitinase signal peptide coding
20 region, and two long single-stranded tails created by treating the linearized pMGS27 with T4 DNA polymerase plus dATP.

The target gene is amplified using polymerase chain reaction ("PCR") or reverse transcriptase-PCR
25 ("RT-PCR") with a pair of oligonucleotides designed to create single-stranded tails that are complementary to the tails of the treated pMGS27, after the PCR fragment has been treated with T4 DNA polymerase and dTTP. A simple annealing can then
30 combine the two molecules into a circular plasmid which is ready to transform the host. Besides being quicker and simpler than the traditional restriction-ligation method of cloning a HA gene into pMGS12, the pMGS27 has the important advantage
35 that it does not yield extra amino acids encoded by the restriction sites created between the chitinase

signal peptide and the mature HA protein. These extra amino acids can sometimes create difficulties such that signal peptidase cannot cleave the signal or that the encoded protein does not fold correctly, as in the case of the B strain HA.

Purification of Recombinant HAO.

Several days post infection, rHAO can be selectively extracted from the peripheral membranes of AcNPV-hemagglutinin infected cells with a non-denaturing, nonionic detergent or other methods known to those skilled in the art for purification of recombinant proteins from insect cells, including, but not limited to affinity or gel chromatography, and antibody binding. The detergent soluble rHAO can be further purified using DEAE ion exchange and lentil lectin affinity chromatography, or other equivalent methods known to those skilled in the art.

In a preferred embodiment, the rHAO is purified using a procedure that is more gentle and results in higher yield of the rHAO from B strains of influenza. This procedure is generally as follows:

The HAO protein which forms an integral part of the membrane of the insect cells is separated from the soluble proteins, the peripheral membrane proteins and the majority of the DNA and RNA by extraction of the cells in a relatively viscous alkaline solution, where an alkaline pH is defined as between about 9.5 and 10.5. Viscosity is increased through the inclusion of sucrose in a concentration of approximately 250 mM. A disulfide-reducing agent, for example, β -mercaptoethanol, is included in a concentration effective to prevent disulfide linking of proteins in the mixture. The cells are suspended in the

extraction buffer, homogenized, and then centrifuged. The pellet is washed by homogenization in a low ionic strength buffer containing a disulfide-reducing agent at an alkaline pH (conductivity is generally less than 1 mS, pH 10.5) and the pellet centrifuged. The HAO is then extracted from the pellet in a buffer containing between 0.3 and 1.5% detergent such as Triton, an amount of disaggregating agent effect to prevent complex formation due to charge interactions, such as between 0.3 and 1.0 M betaine or paurine, at an alkaline pH (9.5 is preferred). The HAO in the supernatant is then purified by anion exchange chromatography followed by cation exchange chromatography. The HAO is applied to the anion exchange column, for example, DEAE or Q-Sepharose® (an agarose bead column with quaternary amine groups), in the same buffer as extracted but diluted at least 1:2 with additional buffer, after equilibration of the column in buffer containing approximately 1/10th the concentration of detergent and disulfide-reducing agent. The HAO is then eluted by lowering the pH to approximately 8.5. The eluted HAO is applied to a cation exchange column in essentially the same buffer. Contaminants are eluted by lowering the pH to approximately 7.4, then eluting the HAO by increasing the salt concentration to 0.15 M NaCl.

This preferred method of purification is described in detail as follows.

Preparation of the recombinant HA-containing membrane fraction. Recombinant HA expressing cells (6.2 g of cells from 0.34 L of culture) are suspended at 100 mg/mL in ice-cold 100 mM sodium pyrophosphate, 100 mM sodium chloride, 250 mM sucrose, 0.1% β -mercaptoethanol, pH 10.5. The

cells are disrupted using a Polytron® homogenizer (Brinkman Instruments Inc., Westbury, NY) at a setting of 4 for 2 min. Alkaline pH of the homogenization medium is needed to increase the solubility of the contaminating proteins and to increase the purity of the membrane preparation. The homogenate is centrifuged for 30 min. at 9,200 g. The supernatant is discarded and the pellet collected. Preparation of the membrane fraction is followed by a low-ionic strength wash step. The pellet is resuspended to the original volume in the ice-cold 0.1% β -mercaptoethanol, 10.5, and homogenized using a Polytron® homogenizer at a setting of 4 for 2 min. The homogenate is centrifuged for 30 min. at 9,200 g. The supernatant is discarded and the pellet collected. This low-ionic strength wash removes additional portion of the peripheral membrane proteins. The preparation of the membrane fraction results in the considerable enrichment in the recombinant HA and in the removal of contaminating nucleic acids.

Extraction of the recombinant HA. The recombinant HA is then selectively extracted from the membrane pellet under conditions that do not denature the antigen. The membrane pellet is homogenized in 41 mL of ice-cold 10 mM ethanolamine pH 9.5, 1% Triton N101, 0.1% β -mercaptoethanol, 25 mM NaCl, 400 mM betaine using a Polytron homogenizer at a setting of 4 for 2 min. After incubation for 40 min. at 23°C, the mixture is centrifuged for 30 min. at 9,200 g. The supernatant containing recombinant HA is decanted and diluted two-fold with the same buffer.

Proteins are analyzed by SDS polyacrylamide gel electrophoresis. Samples are disrupted in a boiling water bath for 10 minutes in the presence

of 2% sodium dodecyl sulfate (SDS) and 5% β -mercaptoethanol, then electrophoresed on an 11% polyacrylamide gel in the presence of 0.1% SDS, then stained with Coomassie blue.

5 **Chromatographic purification.** Chromatographic purification of the recombinant HA was simplified and expensive affinity chromatography on Lentil Lectin Sepharose was eliminated from the process by substitution with a two-step chromatographic
10 purification process which results in a highly purified recombinant HA antigen that is non-denatured and suitable as a component of an influenza vaccine for human use. The chromatography gel matrices used are Pharmacia Q-Sepharose® Fast Flow and CM-Sepharose Fast Flow®.
15

Anion-exchange chromatography. All chromatography is performed at room temperature. The recombinant HA-containing extract prepared as described above is applied at 1 mL/min to Pharmacia
20 Q-Sepharose Fast Flow® (5 mL in a C10/10 Pharmacia column), equilibrated with 10 mM ethanolamine pH 9.5, 0.1% Triton® N101, 0.01% β -mercaptoethanol, 25 mM NaCl, 400 mM betaine. The column is then washed with the equilibration buffer until the UV
25 absorbance of the effluent returns to the baseline. Under these conditions recombinant HA binds to the column while part of the contaminants flow through. Partially purified recombinant HA is then eluted with 30 mM diethanolamine pH 8.5, 0.1% Triton®
30 N101, 0.01% β -mercaptoethanol, 25 mM NaCl, 400 mM betaine.

Cation exchange chromatography. The Q-Sepharose eluate (23 mL) is diluted two-fold with 30 mM diethanolamine pH 8.5, 0.1% Triton® N101,
35 0.01% β -mercaptoethanol, 10 mM NaCl, 400 mM betaine. The column is then washed with 35 mL of

10 mM sodium phosphate pH 7.4, 0.1% Triton® N101,
0.01% β -mercaptoethanol, 10 mM NaCl, 400 mM
betaine. This treatment elutes the contaminants
from the column while recombinant HA remains bound
5 to the CM Sepharose. The detergent is then removed
by washing the column with 10 mM sodium phosphate
pH 7.4, 10 mM NaCl until the UV absorbance of the
effluent returned to the baseline. Purified
recombinant HA is eluted with phosphate buffer
10 saline, pH 7.5 (PBS).

Purified rHA0 is resuspended in an isotonic,
buffered solution. Following the removal of the
detergent, purified rHA0 will efficiently
agglutinate red blood cells.

15 Structural and Biological Properties of
 Recombinant HA0.

rHA0 is purified to at least 95% purity, more
preferably 99% purity. This migrates predominantly
as a single major polypeptide of 68,000 molecular
20 weight on an SDS-polyacrylamide gel. The
quaternary structure of purified recombinant HA0
antigen was examined by electron microscopy,
trypsin resistance, density sedimentation analysis,
and ability to agglutinate red blood cells. These
25 data show that recombinant HA0 forms trimers, which
assemble into rosettes.

Purified rHA0 does not agglutinate cells prior
to removal of detergent, suggesting that the
antigen must form complexes (rosettes) in order to
30 cross-link chicken red blood cells. The
quantitative ability of purified rHA0 to
agglutinate cells is used as a measure of lot-to-
lot consistency of the antigen. One hemagglutinin
unit is defined as the quantity of antigen required
35 to achieve 50% agglutination in a standard
hemagglutinin assay with chicken red blood cells.
Comparative data shows that purified rHA0 antigens

agglutinate red blood cells with an efficiency comparable to that observed with whole influenza virions.

The recombinant HAO can be cleaved at the
5 disulfide bond, causing a conformation change that results in the formation of two chains, HA1 and HA2 as described by Carr, C.M. and Kim, P.S., "A Spring-loaded Mechanism for the Conformational Change of Influenza Hemagglutinin", Cell 73:823-832
10 (1993), which is incorporated by reference herein. Cleavage of recombinant HAO is described in more detail below in Example 6. It is believed that, upon cleavage of natural HAO into HA1 and HA2, the chains become infectious by acquiring the ability
15 to fuse with a cell, thereby creating an improved immune response. The processing of antigens such as influenza hemagglutinin occurs by the binding of antigenic peptides to major histocompatibility (MHC) molecules. The antigen/MHC complex is
20 recognized by T cells to initiate an immune response as described in the review by Harding and Geuze, *Current Opinion in Cell Biology* 5:596-605 (1993), which is incorporated by reference herein. The rHAO produced in a baculovirus, however, is
25 highly stable and immunogenic as the intact molecule. Comparison of the sugar molecules on the HAO expressed in insect cells shows that the glycans are different from those when the HAO is expressed in mammalian or avian cells.

30 Production of Fusion Proteins

Fusion proteins consisting of the HAO fused to a second antigenic protein can be made where the antigenicity of the second protein is low or there are advantages to eliciting an immunogenic response
35 to multiple antigens. An example of a preferred second antigen is the neuraminidase produced by

influenza. The antigen can consist of a cellular, viral, or bacterial protein, or antigenic portion thereof including at least five to eight amino acids. Other antigens include hepatitis B antigen, HIV antigens, and carcinoembryonic antigen. An "immune response", as used herein, refers to either a humoral response, measured by the production of antibody to the antigen, or a cellular response, measured by the elicitation of a T cell mediated response to the antigen. In some cases a "linker" of non-antigenic amino acids may be inserted between the HA and the antigen, to further enhance antigenicity of the antigen as compared to the HA. The process involves constructing a DNA plasmid for fusing target antigen genes to full-length or fragments of the influenza virus HA gene, using oligonucleotide probes and polymerase chain reaction (PCR) methodology.

The HA-target antigen fusion genes are modified for proper expression in insect cells by deletion of the natural hydrophobic signal peptide sequences and replacement with a new baculovirus signal peptide. The fusion gene is introduced into a baculovirus expression vector so that the baculovirus polyhedron promoter directs the transcription of the fusion proteins in infected insect cells. The 18 amino acid baculovirus signal peptide directs the translation of the HA-target antigen fusion polypeptide into the insect cell glycosylation pathway and is not present on the mature fusion protein.

For example, Plasmid pA9440, which contains the A/Beijing/32/92 strain HA gene in the pMGS12 baculovirus transfer plasmid described below, was used as a template for the amplification of the HA gene by polymerase chain reaction (PCR) using the

protocol recommended by the supplier (Gene Amp PCR cloning kit, Perkin Elmer Cetus). The PCR reaction mixture (100 μ l) contained 20 pmol of primers designed to anneal to portions of the HA gene. The 5' and 3' primers were designed with restriction endonuclease sites at the ends that are not found within the HA gene. The 5' PCR primer (O-567) for the HA0 and HA1 fragments begins 52 base pairs downstream from the 5' end of the natural HA gene coding sequences, deleting the natural signal peptide sequence, and adds a *Sma*I site immediately 5' to the HA coding sequences. The 5' PCR primer (O-651) for the HA2 fragment begins at nucleotide 1108 of the natural HA gene, immediately following the codon encoding the arginine residue that is removed during cleavage of HA0 to HA1 and HA2. The 3' PCR primer (O-680) for the HA0 and HA2 fragments was designed to add a *Kpn*I site immediately following the HA coding sequences, removing the natural stop codon. The 3' PCR primer for HA1 (O-679) truncates the gene immediately prior to the arginine residue removed during HA0 cleavage. Amplification of the HA gene fragment was carried out for 30 cycles each consisting of 1 min. at 94°C for denaturation, 2 min. at 55°C for annealing of the primers, and 2 min. at 72°C for extension. The resulting amplified HA gene fragments were electrophoresed on agarose gels, purified from the gel using a GeneClean kit (Bio 101, Inc.), and ligated into a plasmid designed to accept PCR-generated fragments (pCRII; Invitrogen). Thus, plasmids pB142, pB144, and pB330, which contain the HA0, HA1, or HA2 gene fragments, respectively, were obtained.

The HA gene fragments were removed from plasmids pB142, pB144, and pB330 with *Sma*I and *Kpn*I

restriction enzymes and then subcloned by standard recombinant DNA techniques (Sambrook et al., 1989) into the AcNPV transfer plasmid pMGS12. The pMGS12 plasmid contains, from 5' to 3', the AcNPV polyhedron promoter, an ATG initiation codon, the sequence for a cleavable signal peptide from a 61,000 molecular weight baculovirus glycoprotein (61K), *Sma*I and *Kpn*I restriction enzyme cloning sites, and a TAA universal stop codon sequence. Flanking these regulatory regions is DNA from the *Eco*RI I fragment from the AcNPV genome (Summers and Smith, "A manual of methods for baculovirus vectors and insect cell culture procedures". Texas Agricultural Experimental Station Bulletin No. 1555 (1987)). The cloned HA PCR fragments were excised from the pCRII cloning vector with *Sma*I and *Kpn*I, purified with agarose gel electrophoresis and the GeneClean kit, and ligated into pMGS12 that had also been digested with *Sma*I and *Kpn*I. The resulting AcNPV transfer plasmids, pB879, pB1201, and pB1205, contained the coding regions for HA0, HA1, or HA2, respectively, linked in frame with the cleavable baculovirus signal peptide from the 61K gene and the polyhedron promoter. The pB879, pB1201, and pB1205 AcNPV transfer plasmids may be used to fuse HA0, HA1, or HA2 to any gene of interest.

The second step in the construction of HA-CEA fusion gene transfer plasmids was to insert the CEA coding sequences into the HA-encoding constructs. Restriction endonuclease recognition/cleavage sites for *Sma*I and *Kpn*I were placed at both ends of the CEA gene through PCR amplification of plasmid pA9080. The 5' PCR primer, O-649, begins 82 base pairs from the 5' end of the gene, deleting the natural CEA signal peptide sequence. The 3' PCR

primer, O-650, was designed to delete the last 72 basepairs at the 3' end of the gene which codes for the hydrophobic C-terminal region sequence.

Amplification of the CEA gene fragment was carried out for 30 cycles, each consisting of 1 min. at 94°C for denaturation, 2 min. at 55°C for reannealing, and 2 min. at 72°C for extension. The resulting amplified CEA gene fragment was electrophoresed on an agarose gel, purified with the GeneClean procedure, and ligated into pCRII (Invitrogen) according to the manufacturers' instructions. The resulting plasmid, pB806, contains the CEA gene without its natural signal peptide, C-terminal hydrophobic domain, or stop codon, but with both *Sma*I and *Kpn*I sites at both ends of the gene.

A large-scale plasmid prep was performed with the pB806 plasmid, and the DNA was digested either with *Sma*I or *Kpn*I. The CEA-encoding fragments were purified with agarose gel electrophoresis and the GeneClean kit, and the purified fragments were ligated into each of the three HA-encoding constructs (pB879, pB1201, or pB1205) digested with the same restriction enzyme. For example, CEA-encoding fragments with *Sma*I-cut ends were ligated into the HA0-, HA1-, and HA2-encoding constructs (pB879, pB1201, and pB1205, respectively) cut with *Sma*I to create plasmids pB1250, pB1555, and pB1584, respectively. CEA-encoding fragments with *Kpn*I-cut ends were ligated into the HA0-, HA1-, and HA2-encoding constructs cut with *Kpn*I to create pB1264, pB1564, and pB1593. Insertion of the CEA gene at the *Sma*I site placed the CEA coding sequences downstream of the HA coding sequences. For all constructs, the PCR primer were designed such that the EA gene was inserted in-frame with HA, and the fusion gene translation would be terminated at the

universal translation termination signal
(TAATTAATTAA) (Sequence ID No. 4) in the pMGS12
vector sequences downstream of the KpnI site.

5 This construct may be improved by deletion of
intervening amino acids, either between the signal
peptide and HAO, as described below, or between the
HAO and the fusion gene, to enhance folding and
immunogenicity.

Formulation and Packaging of Vaccines

10 The rHA can be formulated and packaged, alone
or in combination with other influenza antigens,
using methods and materials known to those skilled
in the art for influenza vaccines. In a preferred
embodiment, HA proteins from two A strains and one
15 B strain are combined to form a multivalent
vaccine.

In a particularly preferred embodiment, the
HAs are combined with an adjuvant, in an amount
effective to enhance the immunogenic response
20 against the HA proteins. At this time, the only
adjuvant widely used in humans has been alum
(aluminum phosphate or aluminum hydroxide).
Saponin and its purified component Quil A, Freund's
complete adjuvant and other adjuvants used in
25 research and veterinary applications have
toxicities which limit their potential use in human
vaccines. However, new chemically defined
preparations such as muramyl dipeptide,
monophosphoryl lipid A, phospholipid conjugates
30 such as those described by Goodman-Snitkoff et al.
J. Immunol. 147:410-415 (1991) and incorporated by
reference herein, encapsulation of the protein
within a proteoliposome as described by Miller et
al., J. Exp. Med. 176:1739-1744 (1992) and
35 incorporated by reference herein, and encapsulation
of the protein in lipid vesicles such as Novasome™

lipid vesicles (Micro Vascular Systems, Inc., Nashua, NH) should also be useful.

In the preferred embodiment, the vaccine is packaged in a single dosage for immunization by parenteral (i.e., intramuscular, intradermal or subcutaneous) administration or nasopharyngeal (i.e., intranasal) administration. The effective dosage is determined as described in the following examples. The carrier is usually water or a buffered saline, with or without a preservative. The antigen may be lyophilized for resuspension at the time of administration or in solution.

The carrier may also be a polymeric delayed release system. Synthetic polymers are particularly useful in the formulation of a vaccine to effect the controlled release of antigens. An early example of this was the polymerization of methyl methacrylate into spheres having diameters less than one micron to form so-called nano particles, reported by Kreuter, J., Microcapsules and Nanoparticles in Medicine and Pharmacology, M. Donbrow (Ed). CRC Press, p. 125-148. The antibody response as well as the protection against infection with influenza virus was significantly better than when antigen was administered in combination with aluminum hydroxide. Experiments with other particles have demonstrated that the adjuvant effect of these polymers depends on particle size and hydrophobicity.

Microencapsulation has been applied to the injection of microencapsulated pharmaceuticals to give a controlled release. A number of factors contribute to the selection of a particular polymer for microencapsulation. The reproducibility of polymer synthesis and the microencapsulation process, the cost of the microencapsulation

materials and process, the toxicological profile, the requirements for variable release kinetics and the physicochemical compatibility of the polymer and the antigens are all factors that must be considered. Examples of useful polymers are polycarbonates, polyesters, polyurethanes, polyorthoesters and polyamides, particularly those that are biodegradable.

A frequent choice of a carrier for pharmaceuticals and more recently for antigens is poly (d,l-lactide-co-glycolide) (PLGA). This is a biodegradable polyester that has a long history of medical use in erodible sutures, bone plates and other temporary prostheses, where it has not exhibited any toxicity. A wide variety of pharmaceuticals including peptides and antigens have been formulated into PLGA microcapsules. A body of data has accumulated on the adaptation of PLGA for the controlled release of antigen, for example, as reviewed by Eldridge, J.H., et al. Current Topics in Microbiology and Immunology. 1989, 146: 59-66. The entrapment of antigens in PLGA microspheres of 1 to 10 microns in diameter has been shown to have a remarkable adjuvant effect when administered orally. The PLGA microencapsulation process uses a phase separation of a water-in-oil emulsion. The compound of interest is prepared as an aqueous solution and the PLGA is dissolved in a suitable organic solvents such as methylene chloride and ethyl acetate. These two immiscible solutions are co-emulsified by high-speed stirring. A non-solvent for the polymer is then added, causing precipitation of the polymer around the aqueous droplets to form embryonic microcapsules. The microcapsules are collected, and stabilized with one of an assortment of agents

(polyvinyl alcohol (PVA), gelatin, alginates, polyvinylpyrrolidone (PVP), methyl cellulose) and the solvent removed by either drying in vacuo or solvent extraction.

5 The present invention will be further understood by reference to the following non-limiting examples.

10 **Example 1: Propagation and Purification of Influenza Viruses.**

 The following influenza vaccine strains were obtained from the FDA in chicken egg allantoic fluid:

15 A/Beijing/353/89-like (H3N2)
 A/Beijing/32/92-like (H3N2)
 A/Texas/36/91-like (H1N1)
 B/Panama/45/90

20 To propagate the original stock of influenza virus obtained from the FDA, MDCK cells were infected in the presence of TPCK-treated trypsin (Sigma Chemical Co., St. Louis, MO) and fetal bovine serum concentrations optimized to produce
25 the highest titers of first passage virus. The MDCK cells were infected with the influenza strains at a low multiplicity of infection (0.1 to 0.5) as determined by a standard HA assay (Rosen, "Hemagglutination with Animal Viruses" in
30 *Fundamental Techniques in Virology*, ed. K. Habel and N.P. Salzman, pp. 276-28 (Academic Press, New York 1969)). The infected cells were incubated at 33°C for 48 h. and media was assayed for virus production using the hemagglutination activity
35 assay. The conditions yielding the highest HA activity were used to prepare large stocks of influenza virus. The optimum concentrations of TPCK trypsin and fetal bovine serum for the above influenza viruses are listed in Table 1.

Table 1. Optimum Concentration of TPCK Trypsin and Fetal Bovine Serum.

	A/Beijing/ 353/89	A/Beijing/ 32/92	A/Texas/ 36/91	B/Panama /45/90
% Fetal Bovine Serum	0.25%	0.25%	0.25%	5.0%
Amount TPCK Treated Trypsin	45 μ /ml	45 μ g/ml	45 μ /ml	3 μ /ml

Purification of Influenza Virus: Virus was harvested 24-48 hours post infection from 10 T175 tissue culture flasks by clarifying media (1,000 x g for 10 minutes) of influenza infected MDCK cells. 5 The virus was pelleted from the media at 100,000 x g for 1 hour. The resulting viral pellet was resuspended in 1 ml phosphate buffered saline (PBS) pH 7.4 and centrifuged through a 20 ml 20-60% (w/v) sucrose gradient in PBS. The influenza virus band 10 was harvested from the 40-45% sucrose region of the gradient, diluted with PBS and pelleted at 100,000 x g. The purified virus pellet was resuspended in 0.5 ml PBS stored at -70°C.

15 **Example 2: Cloning of Influenza A/Texas/36/91 HA gene.**

A specific example of the cloning step for one of the influenza HA genes is shown in Figure 2. Viral RNA was extracted as described above from 20 Influenza A/Texas/36/91, obtained from the CDC. The universal primer complementary to the 3' end of influenza RNA segments 5'-AGCAAAAGCAGG-3' (SEQ ID NO. 1) was used with murine Maloney Leukemia Virus (M-MuLV) reverse transcriptase to produced 25 influenza cDNAs. Purified viral RNA or mRNA (5 µg) was used as a template to make cDNA utilizing M-MuLV reverse transcriptase supplied in the First-Strand cDNA Synthesis Kit by Pharmacia Inc. The primer used for cDNA of viral RNA from influenza A 30 strains was a synthetic oligonucleotide primer (5'-AGCAAAAGCAGG-3') (SEQ ID NO. 1), which is homologous to the 3' end of all HA gene virion segments.

Amplification of HA genes from cDNA was done 35 by polymerase chain reaction (PCR) using standard reaction conditions (Gene Amp kits; Cetus/Perkin Elmer, Norwalk, CT). The PCR reaction mixture (100

μ l) contained 20 pmol of primers specific for 5' and 3' ends of the HA gene of influenza A (H3) or A (H1) or influenza B strains as determined by consensus sequences found in GenBank DNA data files, as shown in Table 2. Amplification was carried out for 30 cycles with each cycle consisting of 1 minute of denaturation at 94°C, 2 minutes at 55°C for reannealing and 3 minutes at 72°C for extension. The PCR products were analyzed on 0.8% agarose gels for correct size before cloning.

PCR primers from the 5' end of the HA gene: 5'-GGG GGT ACC CCC GGG AGC AAA AGC AGG GGA AAA TAA AAA-3' (SEQ ID NO. 2) and 3' end of the HA gene: 5'-GA AAC GTC ACG TCT TAT ACG/T TAG/T ACT CCA TGG CCC-3' (SEQ ID NO. 3) were used in the PCR to yield the full length HA gene.

A new 5' PCR primer was designed from the 5' end of the gene: 5' end minus signal sequence: 5'-GGG GGT ACC CCC GGG GAC ACA ATA TGT ATA GGC TAC CAT-3' (SEQ ID NO. 4) and the 3' end of the gene: 5'-GA AAC GTC ACG TCT TAT ACG/T TAG/T ACT CCA TGG CCC-3' (SEQ ID NO. 5). These were used in PCR to yield the HA gene minus the signal peptide sequence. This was then inserted into the TA vector cleaved with *Kpn*I. The 61K signal peptide for baculovirus expression and the polyhedrin promoter were then inserted into the TA vector containing the HA gene minus influenza signal peptide sequence. The resulting baculovirus recombination vector contains the polyhedrin promoter, 61K baculovirus signal peptide, and HA gene for Influenza A/Texas/36/91.

HA genes from influenza B strains were cloned from total messenger RNA (mRNA) extracted from MDCK cells infected with the influenza B-strain

B/Panama/45/90. Total RNA was prepared from 5 T175 flasks of infected cells. The harvested cells were lysed in the presence of guanidinium thiocyanate and total cell RNA was purified as described above.

- 5 Total mRNA was extracted from cellular RNA using Oligo-(dT)-cellulose spun columns as described above.

The primer used for mRNA from influenza B strains was a random oligonucleotide DNA primer
10 (Pharmacia, Inc.).

Table 2. Primers Used for PCR Amplification.

A/Beijing/32/93	
5' end gene (SEQ ID NO. 27)	5' GGG <u>GGA TCC GGT ACC AGC AAA AGC AGG GGA TAA TTC TAT</u> 3' BamH1 Kpn1
5' end minus HA signal peptide (SEQ ID NO. 28)	5' GGG <u>GGT ACC CCC GGG GAC TTT CCA GGA AAT GAC AAC AG</u> 3' Kpn1 Sma1
3' end (SEQ ID NO. 29)	3' TAA TTA ATT TTT GTG GGA ACA AAG ATC CTA AGC CAT <u>GGC CC</u> 5' Kpn1
A/Texas/36/91	
5' end gene (SEQ ID NO. 2)	5' GGG <u>GGT ACC CCC GGG AGC AAA AGC AGG GGA AAA TAA AAA</u> 3' Kpn1 Sma1
5' end minus HA signal peptide (SEQ ID NO. 4)	5' GGG <u>GGT ACC CCC GGG GAC ACA ATA TGT ATA GGC TAC CAT</u> 3' Kpn1 Sma1
3' end (SEQ ID NO. 3)	3' GA AAC GTC ACG TCT TAT ACG/T TAG/T ACT <u>CCA TGG CCC</u> 5' Kpn1

Table 2 continued.

B/Panama/45/90	
5' end gene (SEQ ID NO. 30)	5' GGG <u>GAA TTC</u> ACC <u>GGT ACC CCC GGG AAG</u> GCA ATA ATT GTA CTA CTC ATG GT 3' EcoRI KpnI SmaI
5' end minus HA signal peptide (SEQ ID NO. 31)	5' <u>GGT ACC CCC GGG GAT</u> CGA ATC TGC ACT GGG ATA ACA 3' KpnI SmaI
3' end (SEQ ID NO. 32)	3' TG TTA CAA AGA ACA/G AGG TAG ACA GAC ACT CCA TGG CCT AGG CTT AAG GGG 5' KpnI BamHI EcoRI

An example of cDNA synthesis products used influenza virus A/Texas/36/91 viral RNA as a template. The location of the cDNA segments that code for the influenza proteins could be determined as follows. Purified viral RNA was combined in the reaction mixture with the universal single stranded DNA primer 5'-AGCAAAAGCAGG-3' (SEQ ID NO. 1). This primer is complementary to the 3' end of influenza virion segments, as described above. The reaction also contained the addition of [α -³²P]dCTP to visualize the cDNA products which were separated on 1.5% alkaline hydrolysis gel (Maniatis, et al, 1982) and exposed to X-OMAT-AR film.

Example 3: Cloning HA Genes Into Bacterial Plasmids.

The PCR amplified rHA genes were cloned into a pUC-like plasmid vector using the TA Cloning System (Invitrogen, Inc.). The presence of HA genes were verified by restriction enzyme digest analysis of plasmid DNA purified by standard procedures (Maniatis, et al, 1982). The 5' end of the rHA genes were then analyzed by DNA sequencing and new primers were designed to remove the sequences coding for the hydrophobic signal peptides at the N-terminus HA proteins. The specific 5' and 3' oligonucleotide primers listed in Table 2 were then used to amplify cDNA products by PCR and cloned into E. coli TA plasmid vectors (Invitrogen, Inc.) using standard cloning methods. The resulting DNA clones contained coding sequences for the mature HAs.

The rHA genes from A/Texas/36/91, A/Beijing/353/89, A/Beijing/32/92, and B/Panama/45/90 were subcloned by standard procedures (Maniatis et al, 1982) into baculovirus expression vectors. The HA genes were removed from

the TA cloning plasmids with the appropriate restriction enzymes and the purified HA DNA fragment inserted into a baculovirus recombination plasmid. The resulting bacterial clones were
5 screened for ampicillin resistance and then cut with restriction enzymes to release the inserted HA gene to confirm its presence. The recombination plasmids containing HA genes were purified on cesium chloride-ethidium bromide gradients
10 (Maniatis, et al, 1982). The 5' end of the plasmids were sequenced to determine the presence of the correct baculovirus signals (AcNPV polyhedrin promoter, ATG translational start signal and baculovirus signal peptide sequence) and proper
15 HA coding sequence in the correct reading frame. The DNA sequences at the 5' end of the HA genes and flanking AcNPV polyhedrin promoter and baculovirus signal peptide (first 18 amino acids of each amino acid sequence) are shown as SEQUENCE LISTINGS.

20 SEQ ID NO. 6 encodes the 5' end sequence of the HA gene for A/Beijing/32/92 (sequence range 1-481). SEQ ID NO. 7 is the corresponding amino acid sequence (beginning at the start codon "ATG" [nucleotide 21] of SEQ ID NO. 6). The amino acid
25 sequence of the 61K signal peptide is set forth in SEQ ID NO. 7 as amino acids 1-18.

SEQ ID NO. 8 encodes the 5' end sequence of the HA gene for A/Texas/36/91 (sequence range 1-481). SEQ ID NO. 9 is the corresponding amino acid
30 sequence (beginning at the start codon "ATG" [nucleotide 21] of SEQ ID NO. 8). The amino acid sequence of the 61K signal peptide is set forth in SEQ ID NO. 9 as amino acids 1-18.

SEQ ID NO. 10 encodes the 5' end sequence of
35 the HA gene for B/Panama/45/90 (sequence range 1-434). SEQ ID NO. 11 is the corresponding amino

acid sequence (beginning at the start codon "ATG" [nucleotide 21] of SEQ ID NO. 10). The amino acid sequence of the 61K signal peptide is set forth in SEQ ID NO. 11 as amino acids 1-18.

5 In SEQ ID NOs 6, 8, and 10, nucleotides 1-20 are the 3' end of the polyhedrin promoter, nucleotides 21-74 encode the 61K signal peptide, and nucleotides 75 to the end encode the 5' end of the HA gene.

10

Example 4: Expression of Recombinant HA in insect cells.

The chimeric recombination plasmids containing cloned HA genes were purified and 2 μ g was mixed
15 with 1 μ g AcNPV wild type DNA. The DNAs were co-precipitated with calcium and transfected into *S. frugiperda* cells using standard procedures (Smith, Summers, and Fraser, Mol. and Cell. Biol. 3:2156-2165 (1983)). Recombinant baculoviruses
20 were identified on the basis of plaque morphology then further purified by additional rounds of plaque-purification. Plaque-purified recombinant baculoviruses are screened for expression of rHA and a single baculovirus expression vector was
25 selected for further development.

S. frugiperda cells were infected with a baculovirus vector containing the HA gene from the Influenza strain: B/Panama/45/90. At 24, 48, and 72 hours post infection, 1 X 10⁶ cells were pulsed
30 with 25 μ Ci [³⁵S]methionine for 15 minutes to label proteins being synthesized. The cells were collected and the proteins separated on an 11% polyacrylamide gel in the presence of 0.1% SDS. The radiolabeled proteins were detected by exposure
35 to X-OMAT-AR film. The location of protein standards and their size in kilodaltons (kd) indicated that the 85 kd recombinant HA protein is

one of the major proteins being synthesized in the cells at 48 hours and 72 hours post infection.

Example 5: Production and Purification of Recombinant HA

5

The baculovirus expression vector A8611, which contains the gene for influenza A/Beijing/353/89, produced essentially as described above for A/Beijing/32/92 hemagglutinin under the control of the polyhedrin promoter, was used to infect *S. frugiperda* cells. Cells were grown at 27°C to a density of 1×10^6 cells/mL in TNMFH media (Gibco BRL, Gaithersburg, MD) supplemented with 10% fetal bovine serum, and infected at a multiplicity of infection (MOI) of 1 with the A8611 recombinant baculovirus. During infection the influenza A/Beijing/353/89 hemagglutinin is produced under the transcriptional control of the baculovirus polyhedrin promoter. Cells are harvested 72 hours post-infection by centrifugation for 15 minutes at 3,400 x g, and washed by resuspension in serum-free TNMFH media followed by centrifugation for 30 minutes at 10,400 x g. The supernatant is decanted, and infected cell pellets are stored at -70°C.

25

A process was developed in which the recombinant HA is selectively extracted from the infected cells under conditions that do not denature the antigen. Unless noted, all extraction steps are performed at 4°C. The cell pellet from 0.5 L of culture (approximately 5×10^8 cells) was disrupted for 2 minutes in 40 mL of ice-cold 30 mM Tris-HCl, pH 8.4, 25 mM LiCl, 1% (v/v) Tween-20, 1 mg/mL leupeptin, using a Polytron™ homogenizer (Brinkmann Instruments Inc. Westbury, NY). The homogenate was centrifuged for 30 minutes at 9,200 x g. The supernatant was discarded, and the pellet

35

collected. This step removes soluble and peripheral membrane proteins from the insect cells without extraction of integral membrane proteins like rHA. To extract the rHA the pellet was

5 homogenized for 2 minutes at a setting of 4 in 40 mL of ice-cold 30 mM Tris, 10 mM ethanolamine, pH 11, 25 mM LiCl, 2% Tween-20. After a 60 minute incubation on ice, the pH of the homogenate was adjusted to 8.4 with 1 N HCl, and insoluble

10 material was removed by centrifugation for 30 minutes at 9,200 x g. The supernatant containing the soluble rHA was decanted, and the pH was checked and, if necessary, adjusted to 8.4 at room temperature. The insoluble material was

15 resuspended in 40 mL of water for analysis. The HA integral membrane protein was solubilized under the high pH, Tween-20 detergent conditions and remains in solution after the pH is dropped.

Proteins were analyzed by SDS polyacrylamide

20 gel electrophoresis. Samples were disrupted in a boiling water bath for 10 minutes in the presence of 2% sodium dodecyl sulfate (SDS) and 5% beta-mercaptoethanol, then electrophoresed on an 11% polyacrylamide gel in the presence of 0.1% SDS,

25 then stained with Coomassie blue.

A chromatography purification process was developed to purify recombinant HA which results in a highly purified recombinant HA antigen that is non-denatured and suitable as a component of an

30 influenza vaccine for human use. The following procedure was used to purify the A/Beijing/353/89 HA from *S. frugiperda* cells infected with the recombinant virus A8611.

The chromatography gel matrices used to purify

35 HA from 0.5 L of infected *S. frugiperda* cells were 30 mL Pharmacia DEAE Sepharose Fast Flow (in a

Pharmacia C16/20 column) and a 4 mL Pharmacia
Lentil Lectin Sepharose 4B (in a Pharmacia C10/10
column). The outlet of the DEAE column is
connected to the inlet of the lentil lectin column,
5 and the S/N 2 cell extract prepared as described
above was applied to the coupled columns at a flow
rate of 1 mL/minute. The columns were washed with
30 mM Tris-HCl, pH 8.4, 25 mM LiCl, 0.5% Tween-20
until the UV absorption at 280 nm of the lentil
10 lectin effluent returns to baseline. Under these
conditions most of the contaminating proteins bind
to DEAE but recombinant HA flows through the
column. The remaining contaminants pass through
the lectin column and glycosylated rHA binds to the
15 lentil lectin affinity matrix. The DEAE column is
disconnected, and the lectin column is washed with
another 40 mL of 30 mM Tris-HCl, pH 8.4, 25 mM
LiCl, 0.5% Tween-20. Next, the lectin column is
washed with 40 mL of 30 mM Tris-HCl, pH 8.4, 25 mM
20 LiCl, 0.4% (v/v) sodium deoxycholate (DOC). This
step replaces the Tween-20 detergent with a
detergent, like DOC, that can be removed from the
protein by dialysis. Recombinant HA is then eluted
from the lectin column with approximately 20 mL of
25 40 mL of 30 mM Tris-HCl, pH 8.4, 25 mM LiCl, 0.4%
(v/v) sodium deoxycholate containing 0.3 M α -D-
methyl mannoside. Results are analyzed by 11%
PAGE.

Due to the genetic variability of influenza HA
30 proteins, the details of the above purification
process may vary with each unique recombinant HA
protein. For example, the rHA may bind to the DEAE
ion exchange column instead of flowing through.
Should this occur, the rHA would be removed from
35 the DEAE column with by washing the column with

buffer containing higher concentration of LiCl, NaCl, or other salts.

To remove the DOC detergent and other buffer components, the eluate from the lectin column
5 containing the purified rHA was dialyzed against phosphate buffered saline, pH 7.5 (PBS). The purified recombinant HA was at least 95% pure as determined by analysis on SDS polyacrylamide gels.

10 **Example 6: Analysis of rHA Protease Resistance.**

Mature HA assembles into trimeric structures which are resistant to a variety of proteases, including trypsin, that degrade HA monomers (Murphy and Webster, 1990). Resistance to trypsin
15 treatment can therefore be used as an assay for functional trimer formation. The following procedure was used to study resistance of rHA to protease treatment.

Two aliquots of purified rHA
20 (A/Beijing/353/89) at 60 µg/mL were incubated on ice for 30 minutes in 30 mM Tris-HCl, pH 8.4, 150 mM NaCl, in the presence and absence of 50 µg/mL TPCK-treated trypsin. The reaction was stopped by the addition of 57.4 mM phenyl methyl sulfonyl
25 fluoride in isopropanol to a final concentration of 1 mM. Aliquots of each sample were denatured by boiling in 3% SDS under reducing conditions, electrophoresed on 11.5% polyacrylamide gels, and transferred to nitrocellulose filter using standard
30 Western blotting procedures. The HA polypeptides were detected using guinea pig anti-HA serum prepared against purified rHA and a goat anti-guinea pig IgG alkaline phosphatase conjugate.

Untreated rHA migrates at the size of the HA
35 precursor (HA0). Protease treatment results in two major bands that migrate at the sizes predicted for

influenza hemagglutinin HA1 and HA2. The results show that trypsin cleaves the rHA protein once to produce two polypeptides that are the sizes predicted for HA1 and HA2. No further proteolytic processing occurs. These results demonstrate that rHA purified by the above process is resistant to degradation by protease. This property is consistent with purified rHA being in the form of trimers.

10

Example 7: Immunogenicity of rHA using standardized Mouse Potency Assay.

One approach to measure immunogenicity of an antigen is to determine the quantity necessary to induce a detectable antibody response in mice (mouse potency assay). A standardized mouse potency assay is used to measure the immunogenicity of rHA0 vaccine. Groups of 5-10 mice are immunized once with vaccine containing serial dilutions of rHA, i.e., 0.500 μ g, 0.1 μ g, 0.02 μ g, and 0.004 μ g purified rHA. Sera are collected 28 days post immunization and antibodies against the rHA antigen measured in a standard enzyme-linked immunological solid-phase assay (ELISA) in 96 well microtiter plates. A mouse has seroconverted if the OD450 at a 1:100 dilution of the 28 day antisera is greater than three standard deviations above the mean of the OD450 of mouse pre-immune sera. The effective dosage of vaccine needed to seroconvert 50% of the mice (ED50) is a measure of the immunogenicity of the antigen.

For example, four groups of 10 mice are immunized once with either 0.1 μ g, 0.02 μ g, 0.004 μ g, or 0.0008 μ g (5-fold dilutions) of rHA0 vaccine. Sera are collected 28 days post immunization and measured against each rHA0 antigen in the vaccine for seroconversion in an ELISA

assay. The dosage needed to seroconvert 50% of the mice (ED_{50}) is calculated and a minimum ED_{50} established for each rHA0 antigen.

Preliminary data shows that a single dose of
5 0.004 μ g of rHA0 will seroconvert at least 50% of the mice.

Example 8: Administration of rHA in combination with an Adjuvant and comparison with available influenza vaccines.
10

The mouse potency of purified rHA from influenza A/Beijing/353/89 was tested with alum or without alum (neat) and compared to a commercial influenza vaccine, FLUZONE® (Connaught
15 Laboratories, Inc. Swiftwater, PA) which contains the A/Beijing/353/89 strain of influenza. Vaccine was administered in a dosage of 0.5 μ g, 0.1 μ g, 0.02 μ g, and 0.04 μ g. The mice were boosted at
20 day 28 with the doses of purified rHA described above. On day 42 sera were collected and titered in an ELISA assay for IgG anti-HA antibodies.

The results are shown in Figure 3. In the absence of adjuvant, only a dosage of 0.5 μ g induced production of significant antibody titer
25 (200,000). In the presence of adjuvant, dosages of as little as 0.004 μ g of rHA0 produced significant antibody. The animals immunized with rHA (neat) produced approximately the same levels of anti-HA antibodies as the commercial vaccine. Alum
30 increased the immunogenicity of rHA, and anti-HA titers were generated that were 10-fold or higher than without adjuvant.

In summary, comparison of the immunogenicity of purified rHA0s with an influenza whole virion
35 vaccine, (FLUZONE®, Connaught Laboratories, Inc., Swiftwater, PA), demonstrates that rHA0 elicits a similar immune response in mice over a period of 42

days. Adsorption of the rHA0 to alum significantly increases the immunogenicity of the purified rHA0 in mice, as measured by the assay described in Example 7. The combination with alum elicits IgG
5 hemagglutinin antibodies that are higher than the Fluzone® influenza vaccines.

Example 9: Hemagglutination Inhibition Studies.

Hemagglutination inhibition (HAI) antibodies
10 bind to three of four known epitopes on hemagglutinin and block the ability of influenza to agglutinate red blood cells (Wilson et al, "Structure of the hemagglutinin membrane glycoprotein of influenza virus at 3A° resolution".
15 Nature, 289:366-378 (1981)). These antigenic determinants are clustered around the sialic acid receptor binding site on hemagglutinin trimers. Antibodies against these sites will neutralize virus infectivity (Weis, et al., "Structure of the
20 influenza virus hemagglutinin complexed with its receptor, sialic acid", Nature 333:426-431 (1988)). The titer and specificity of HAI antibodies are an important measure of the potential for an influenza vaccine to protect against infection with like and
25 related strains of influenza.

Studies were conducted in mice comparing the ability of purified rHA0 from A/Beijing/353/89 and FLUZONE® (Connaught Laboratories, Inc., Swiftwater, PA) to elicit HAI antibodies. Groups of 5 mice
30 were injected on days 0 and 28 with 0.5 µg, 0.1 µg, 0.02 µg, or 0.004 µg of rHA0 or three times these quantities of FLUZONE® hemagglutinin so that equal levels of recombinant or viral A/Beijing/353/89 hemagglutinin were administered. For example, mice
35 in the highest dose group were immunized with 1.5 µg of FLUZONE® hemagglutinin (0.5 µg of

hemagglutinin from each strain) and 0.5 μ g rHA0. The presence of additional hemagglutinin antigen in FLUZONE[®] from two other influenza strains may result in some cross-reactive antibodies.

5 Anti-hemagglutinin antibodies (hemagglutinin IgG) were measured in a standard dilutional ELISA against purified rHA0. HAI antibodies were measured against 4 hemagglutinin units of the following antigens: whole influenza

10 A/Beijing/353/89 virus (A/Bei), purified rHA0 A/Beijing/353/89 antigen, and FLUZONE[®]. The HAI titer is the reciprocal of the highest dilution of antisera which inhibits the agglutination of chicken red blood cells by 50%.

15 Table 3 summarizes serum hemagglutinin IgG and HAI titers in the mice at day 42. High levels of anti-hemagglutinin antibodies were produced with the recombinant rHA0 vaccine. These were about ten fold higher titers than FLUZONE[®]. Most significant
20 is that the rHA0 vaccine produced good titers of antibodies that block agglutination of red blood cells by the A/Beijing/353/89 virus and rHA0 antigens. Thus, the rHA0 vaccine produced HAI antibodies that recognized equally well the
25 immunogen and the influenza A/Beijing virus. The lower HAI titers against FLUZONE[®] may be due to the inability of the antisera to block agglutination by the other two strains of hemagglutinin in the FLUZONE[®] vaccine. In contrast, FLUZONE[®] immunized
30 mice produce high HAI antibodies when measured only against itself. The HAI titers against influenza A/Beijing/353/89 virus and the rHA0 antigen were considerably reduced. Similar patterns were observed in the mice in the lower dose groups.

Table 3. HAI Titters against rHA0 and FLUZONE®

Mouse #	rHA0 A/Bei (day 42)				FLUZONE® (day 42)			
	HA IgG		HAI		HA IgG		HAI	
	rHA0	A/Bei	rHA0	FLUZONE	rHA0	A/Bei	rHA0	FLUZONE
1	4,096,000	1,920	960	15	256,000	<10	<10	600
2	4,096,000	480	480	15	512,000	120	120	600
3	8,192,000	1,920	960	15	256,000	60	60	300
4	4,096,000	960	960	30	128,000	30	30	400
5	4,096,000	1,920	960	60	512,000	80	80	400
MEAN	4,915,000	1,440	864	27	332,800	58	58	460

These data also suggest that there are genetic differences between the influenza A/Beijing/353/89 strain in FLUZONE® and this same strain of influenza obtained from the FDA and passaged once in eggs prior to using the HAI assay. The fact that antibodies produced in response to the recombinant HA0 cloned from influenza A/Beijing/353/89 blocks agglutination of red blood cells by this strain of influenza as well as itself is good evidence that there were no genetic changes during the cloning process that effected the sialic acid receptor binding site on the purified rHA0 antigen.

Example 10: Formulation and Clinical Efficacy of a 1993/1994 Influenza Vaccine.

A series of human clinical trials was conducted to characterize the safety and immunogenicity in humans of an experimental influenza vaccine containing recombinant HA and to obtain preliminary data regarding the protective efficacy of such a vaccine against natural infection during an epidemic season. The results demonstrate that vaccines containing the recombinant influenza hemagglutinin (rHA0), produced in accordance with the methods described herein surprisingly caused fewer local adverse reactions and provided an equivalent or superior protective immune response when compared to a commercially available, licensed attenuated flu vaccine produced in eggs.

MATERIALS AND METHODS

Vaccines. The recombinant HA vaccines used in this study contained full length uncleaved HA (HA0) glycoprotein from the influenza A/Beijing/32/92 (H3N2) virus. Recombinant HA0 (rHA0) was produced in cultures of Lepidopteran (insect) cells

following exposure to a baculovirus vector containing cDNA inserts encoding the HA gene. The expressed protein was purified under non-denaturing conditions to >95%, as measured by quantitative scanning densitometry of the bulk antigen electrophoresed on sodium dodecyl sulfate-polyacrylamide gels. The identity of the peptide was confirmed by amino acid analysis, N-terminal sequencing and Western blot analysis with anti-influenza A/Beijing/32/92 sera. The rHA0 vaccines contained a specified amount of the synthetic HA antigen either dissolved in a phosphate-buffered saline solution or adsorbed to aluminum phosphate (alum) adjuvant in the form of a gel suspension. The licensed trivalent subvirion vaccine used in this study contained 15 µg/dose of each the HAs from influenza A/Texas/36/91 (N1N1), A/Beijing/32/92 (H3N2) and B/Panama,45/90 viruses (FLUZONE™ attenuated flu vaccine produced in eggs, Connaught Laboratories, Swiftwater, PA).

Clinical Studies. Identical study protocols were approved by the Institutional Review Boards of Saint Louis University and the University of Rochester. Healthy adults aged 18 to 45 years were enrolled at both institutions. Subjects were randomly assigned to receive one of the following five vaccine preparations in a double-blinded manner: (1) 15 µg rHA0, (2) µg rHA0 plus alum, (3) 90 µg rHA0, (4) licensed trivalent inactivated influenza vaccine, or (5) saline placebo. Vaccines were administered by intramuscular injection in a volume of 0.5 ml. To allow for an initial assessment of the safety of the three vaccine preparations containing rHA0, the first 25 subjects to be vaccinated were randomized (i.e., 5 persons per study arm) independently of the other subjects

and closely monitored by phone contact for 48 hours post-vaccination before proceeding with the remaining vaccinations. All subjects were instructed to fill out a daily report card of adverse reactions, including both local and systemic symptoms, during the first 6 days post-vaccination. Symptoms were self-graded as mild, moderate or severe in nature. Oral temperatures were taken and recorded by participants if they felt feverish. If present, localized swelling or erythema at the injection site was graded according to whether the area was less than or greater than the size of a quarter in diameter, respectively. All vaccinations were performed during the last week of November and first week of December, 1993. Serum specimens were obtained from each subject at the time of vaccination, 3 weeks post-vaccination, and once again in late March or April 1994 at least 2 to 3 weeks after influenza viruses were no longer circulating in the local communities. Volunteers at each institution were instructed to contact the study center if they experienced an influenza-like illness during the winter influenza epidemic season. An influenza-like illness was defined as the presence of any respiratory symptom(s) of two days or greater duration accompanied by fever and/or systemic symptoms of myalgias or chills. Subjects who reported influenza-like symptoms had nasal and pharyngeal swabs obtained for virus culture and identification. Clinical specimens were given coded identification numbers and processed in a blinded fashion.

Serology. For each type of serologic assay, all specimens from both institutions were tested in one batch by a single laboratory. Hemagglutination inhibition (HAI) antibodies to influenza

A/Beijing/32/93 (H3N2) virus antigen were measured in sera by a standard microtiter assay, following removal of nonspecific inhibitor with receptor destroying enzyme and of cold agglutinins by hemadsorption at 4°C. The titer was defined as the highest serum dilution that completely prevented hemagglutination by 4 antigen units of virus, using 1:4 as the starting dilution. Serum HA-specific immunoglobulin G (IgG) antibodies were measured by enzyme-linked immunosorbent assay (ELISA), using purified rHA0 from influenza A/Beijing/32/92 (H3N2) as the coating antigen. The sequence of reagents from solid phase outward consisted of (1) purified rHA0 antigen, (2) serum specimen, (3) alkaline phosphatase-conjugated goat anti-human IgG, and (4) p-nitrophenyl phosphate disodium substrate. The ELISA titer was expressed as the highest dilution at which the optical density of the antigen-containing well was at least twice that of the corresponding control well without antigen. Neutralizing antibodies were measured using the microneutralization assay previously described by Treanor, J.J., and Betts, R.F., *J. Infect. Dis.* 168:455-459 (1993). In brief, serial dilutions of heat-inactivated sera were mixed with approximately 100 TCID₅₀ of influenza A/Beijing/32/92 (H3N2) virus and incubated at 37°C for 1 hr. The virus-sera mixture was then adsorbed to confluent monolayers of Madin-Darby canine kidney (MDCK) cells in 96-well plates for 1 hr at room temperature. The plates were washed to remove residual inoculum, refed serum-free Dulbecco's MEM with 2 µg/ml trypsin, and incubated in 5% CO₂ at 33°C for 72 hr. Cells were then fixed with methanol, and viral replication was assessed using a panel of murine monoclonal antibodies specific for the matrix and

nucleoproteins of influenza A virus (Centers for Disease Control, Atlanta, GA), followed by alkaline phosphatase-conjugated anti-mouse IgG. The end-point titer of the sera was defined as the highest dilution resulting in greater than 50% reduction in signal compared with nonneutralized control wells.

Virology. Viral cultures of nasopharyngeal swab specimens were performed at each institution by standard techniques. Specimens were inoculated in either MDCK or rhesus monkey kidney cells and incubated at 33°C for 14 days. Hemadsorption of cell monolayers was tested with 0.4% guinea pig erythrocytes. Influenza viruses were identified in hemadsorption positive cultures by HAI using H3-specific antisera (Centers for Disease Control).

Statistical Analyses. Reciprocal HAI, ELISA IgG and neutralizing antibody titers were logarithmically transformed for statistical analysis. A significant response to vaccination was defined as a fourfold or greater rise in antibody titer between the pre-vaccination and 3-week post-vaccination serum specimens. Laboratory evidence of influenza A (H3N2) virus infection was defined as the isolation of virus from nasopharyngeal secretions and/or a four-fold or greater increase in serum HAI antibody titer between the 3-week post-vaccination (preseason) specimen collected in December and the corresponding postseason specimen collected the following spring. Differences between vaccine groups were analyzed using Fisher's exact test to compare the proportions of subjects with adverse reactions, significant antibody responses or laboratory-confirmed influenza illness or infection, and analysis of variance (ANOVA) to compare post-vaccination mean reciprocal log₂

antibody titers. The modified Bonferroni's inequality and Tukey-Kramer tests were applied where appropriate to account for multiple possible comparisons.

5 RESULTS

Reactogenicity. The rHA0 vaccines used in this study were safe and well-tolerated. The frequency of adverse reactions did not appear to be influenced by changing the dose of rHA0 antigen
10 from 15 μ g to 90 μ g, but may have been slightly increased by the addition of alum. Localized erythema, pain and tenderness at the injection site were each reported significantly more frequently by recipients of licensed subvirion vaccine than by
15 recipients of either 15 μ g or 90 μ g rHA0 in saline. With the exception of one individual who experienced moderately severe pain, tenderness and stiffness in the arm following immunization with licensed vaccine, all symptoms were graded as mild
20 in nature and were generally 1-2 days in duration. Localized erythema and/or induration, when present, was invariably less than the area of a quarter in size.

Immunogenicity. Baseline titers of serum HAI
25 antibody to influenza A/Beijing/32/92 (H3N2) virus were less than or equal to 1:8 in 64 (50%) of the 127 subjects enrolled. Most subjects in each of the four vaccine groups had HA-specific serologic responses measured by HAI and ELISA (Table 4).
30 Post-vaccination titers of serum HAI antibody were greater than or equal to 1:32 in all vaccine recipients with the exceptions of two persons given 15 μ g rHA0 and one given the licensed vaccine. Vaccination was likewise associated with the
35 production of neutralizing antibody in the majority of volunteers. Mean rises in antibody titers and

seroconversion rates tended to be slightly lower following immunization with 15 µg rHA0 than with licensed vaccine, although these differences were not statistically significant. Antibody response to rHA0 were not enhanced by the addition of alum. Subjects immunized with 90 µg rHA0 achieved post-vaccination mean HAI and ELISA IgG antibody titers that were two- to five-fold higher than in any of the other three vaccine groups (differences were statistically significant when comparing serum HAI titers).

Protective Efficacy. During the period of surveillance, there were a total of 28 influenza-like illnesses reported by 26 subjects. Four of these individuals (three of whom had received placebo and one of whom had been immunized with 15 µg rHA0) had influenza A (H3N2) virus isolated from nasopharyngeal cultures. Significant increases in HAI antibody titer to influenza A/Beijing/32/92 (H3N2) between preseason and postseason serum specimens were also present in three of the four culture-confirmed cases, but not in any other individuals who reported illness. The lone rHA0 recipient who subsequently developed laboratory-confirmed influenza illness had the positive culture obtained 31 days after immunization, and had seroconverted from a prevaccination HAI titer of less than 1:4 to a post-vaccination (preseason) titer of 1:32. Two additional placebo recipients and one volunteer immunized with licensed vaccine had serologic evidence of infection with influenza A (H3N2) virus during the epidemic season in the absence of clinical illness. Compared to all vaccinated subjects (or to all subjects who received any rHA0 vaccine) as one group, a significantly larger proportion of placebo

recipients had laboratory-confirmed influenza A (H3N2) illness ($p < .05$) or infection ($p < .005$).

The above findings indicate that influenza vaccines containing purified rHA0 antigen, prepared as described in the above-identified patent application, are well-tolerated and capable of eliciting protective immune responses in human subjects. Even at a dose of 90 μg , the rHA0 evaluated in this study was no more reactogenic than saline placebo, and caused significantly fewer local adverse reactions than did a licensed trivalent subvirion vaccine containing half as much (i.e., 45 μg) total HA antigen.

Neutralizing, HA-specific antibody responses to the 15 μg rHA0 preparation were comparable to those elicited by subvirion vaccine, and were significantly improved by raising the dose of rHA0 to 90 μg .

Overall rates of infection and illness resulting from natural exposure to the circulating epidemic strain of influenza A (H3N2) virus were significantly lower among vaccinated subjects than among placebo recipients. The data suggest that protective immunity conferred by rHA0, particularly when administered at high doses, is comparable or superior to that induced by currently available vaccines.

Table 4: Serum antibody responses in young adult subjects following immunization with vaccines containing purified recombinant hemagglutinin (rHAO) from influenza A/Beijing 32/92 (H3N2), licensed trivalent trivalent subviroon containing 15 µg HA from A/Beijing/32/92 (H3N2), or saline placebo.

Vaccine (Number in group	HAI antibody			ELISA IgG HA antibody			Neutralizing antibody Microneutra- lization titer %with Pre Post ≥ 4x rise		
	HAI titer Pre Post	%with Post	% with post ≥1:32	ELISA titer Pre Post	%with Post ≥4x rise				
rHAO 15 µg (26)	3.7±0.3	9.0±0.6*	85	92	8.7±0.3 12.0±0.3	88	5.7±0.3 10.0±0.4		85
rHAO 15 µg plus alum (26)	4.3±0.5	8.6±0.4*	88	100	9.4±0.4 11.5±0.4	76	6.4±0.4 9.3±0.2		76
rHAO 90 µg (26)	3.3±0.4	11.1±0.3	100	100	8.5±0.4 13.1±0.4	100	5.7±0.3 10.2±0.4		96
Licensed subviroon (26)	3.7±0.4	9.3±0.5*	100	96	8.1±0.4 12.0±0.4	92	5.8±0.3 9.9±0.4		96
Placebo (24)	3.7±0.5	3.8±0.5*	0	38	9.1±0.3 9.1±0.3	0	5.3±0.4 5.4±0.4		8

HAI, hemagglutination inhibition; HA, hemagglutinin; ELISA, enzyme-linked immunosorbent assay. Postvaccination serum specimens were obtained three weeks after immunization. Antibody titers are expressed as means reciprocal log₂SEM. Statistical comparisons are made between the mean postvaccination HAI titer of the designated group and that of the 90 µg rHAO vaccine group by analysis of variance with Dunnett's test for multiple comparisons. *, P<0.01; +, P<0.05; #, P<0.01

Example 11: Method for making an improved HAO cloning vector.

An improved cloning vector for expression of mature HA wherein the gene encoding the HA was located immediately downstream of the sequence encoding the chitinase signal peptide was designed.

Linear pMGS27 with Single-stranded Tails was created

In the pMGS12 plasmid, HA was cloned into *Sma*I or *Kpn*I sites immediately downstream from the chitinase signal peptide. The nucleic and amino acid sequences are shown respectively as SEQ ID NO. 22 and SEQ ID NO. 23:

5'- chitinase signal peptide *Sma*I *Kpn*I
 TGG TTG GTC GCC GTT TCT AAC GCG ATT CCC GGG GGT ACC
 TRP LEU VAL ALA VAL SER ASN ALA ILE PRO GLY GLY THR

This region was changed by oligo directed mutagenesis to create pMGS27 (changed bases were underlined) (SEQ ID NO. 24):

5'-
 TGG TTA GTC GCC GTG TCCTGCAGGCCAGAGAGGCCTT GGT ACC
*Pst*I

Plasmid pMGS27 was linearized with *Pst*I cut (residues 6-35 of SEQ ID NO. 24 shown):
 A GTC GCC GTG TCC TGCA 5' GGCCAGAGAGGCC T
 T CAG CGG CAC AGG 5' ACGTCCGGTCTCTCCGG A
 then treating the linear pMGS27 with T4 DNA polymerase plus dATP to create single stranded tails as shown below (residues 23-36 and complement of residues 6-18 of SEQ ID NO. 24):

A 5' GGCCAGAGAGGCC T
 T CAG CGG CAC AGG 5' A

Target HA Gene was Cloned into pMGS27
 Step 1. PCR primers were synthesized.
 Forward oligo (SEQ ID NO. 25):

62

5' GTC GCC GTG TCC AAC GCG (5' end 20 bases of the mature HA)

Reverse oligo (complement of SEQ ID NO. 26):

(3' end 20 bases of the mature HA) ATT AA

5 CCGGTCTCTCCGG 5'

PCR of the HA gene

PCR of the target HA gene with the two oligos was used to obtain (SEQ ID NO. 25 and SEQ ID NO. 26):

10 5' GTC GCC GTG TCC AAC GCG (mature HA)
CAG CGG CAC AGG TTG CGC (mature HA)

TAA TTGGCCAGAGAGGCC 3'
ATT AACCGGTCTCTCCGG

15 Anneal target HA gene into pMGS27 and transform E.coli

Linear pMGS27 and the T4 DNA polymerase treated PCR fragment of the HA gene were mixed. The two molecules anneal to each other, to form a
20 circular plasmid which is ready to be used for transforming *E. coli*. The diagram includes SEQ ID NOS. 25 and 26, residues 23-36 and 6-18 of SEQ ID NO. 24.

25 GTCGCCGTGTCCAACGCG (mature HA) TAATT
TTGCGC (mature HA) ATTAACCGGTCTCTCCGG

+

30 A GGCCAGAGAGGCCT
TCAGCGGCACAGG A

to

35 chitinase signal peptide stop
GTCGCCGTGTCCAACGCG (mature HA) TAATTGGCCAGAGAGGCCT

As shown above, there is no extra amino acid in between the signal peptide and the mature HA.

40 **Example 12: Preparation and efficacy of a Trivalent Types A and B 1995-1996 Influenza Virus Vaccine.**

Influenza virus vaccine, purified recombinant hemagglutinin, trivalent, types A and B

Influenza virus vaccine, purified recombinant hemagglutinin, trivalent, types A and B (A/Texas/36/92\1 (H1N1), A/Johannesburg/33/94 (H3N2), and B/Harbin/7/94) is a non-infectious subunit derived from purified, recombinant influenza hemagglutinin antigens (HA). The HA genes were cloned from the Center for Disease Control/Food and Drug Administration recommended strains of influenza A and B viruses as described above and the identity of each cloned gene determined by DNA sequence analysis. Baculovirus expression vectors containing the cloned HA genes from influenza virus strains A/Texas/36/91 (H1N1), A/Johannesburg/33/94 (H3N2), B/Harbin/7/94 were used to produce the recombinant HA antigens in cultured insect cells. The recombinant HA proteins are full length, uncleaved hemagglutinins (rHAO) with a molecular weight of approximately 69,000. The rHAO were produced in a *Spodoptera frugiperda* (Lepidopteran) cell line maintained in a serum-free culture medium. The trivalent vaccines is composed of purified (greater than 95% pure, more probably greater than 99% pure) rHAO from the two influenza A strains and one B strain mixed in equal proportions. The vaccine is supplied for clinical use as purified types A and B rHAO proteins in phosphate buffered saline solution without added preservative.

Animal studies with monovalent, bivalent and trivalent rHAO vaccines have demonstrated that they are free of significant toxicity. There are no detectable toxic or adventitious agents in the vaccine. General safety and immunogenicity studies of A/Beijing/32/92 and A/Texas/36/91 rHAO were conducted in mice and guinea pigs. No adverse reactions were noted. In mice, a single

immunization with 15 micrograms of rHAO antigens without adjuvant induces in two to three weeks high levels of anti-HA IgG antibodies, hemagglutinin inhibition (HAI) antibodies and neutralizing
5 antibodies.

In one study, groups of ten mice were immunized with 15 micrograms of purified rHAO A/Beijing/32/92 (H3N2) made in cells adapted to media containing 10% fetal bovine serum or rHAO
10 made in insect cells adapted to media containing 10% fetal bovine serum or rHAO made in insect cells adapted to a serum-free medium (rHAO-SF). Two and three weeks post injection the mice were bled and serum samples prepared. Each sera were measured
15 for anti-HA IgG and HAI antibodies. Both rHAO and rHAO-SF antigens elicit similar titers of anti-HA and HAI antibodies. Both rHAO and rHAO-SF antigens elicit similar titers of anti-HA and HAI
20 antibodies. Two weeks following the single immunization, most of the mice have significant titers of HAI antibodies and by week three 8/10 mice in each group had HAI titers of 32 or greater. These and other biochemical and immunological
25 studies demonstrate that rHAO produced in serum-free insect cell culture is indistinguishable from rHAO manufactured under serum-containing fermentation conditions.

A study was conducted to compare the 1994-1995 formulation of the trivalent rHAO influenza vaccine
30 with a licensed purified virus surface antigen vaccine, Fluvirin® (an attenuated influenza viral vaccine produced by culturing in eggs). Each vaccine contained 15 micrograms rHAO or viral HA per 0.5 ml from A/Texas/36/91 (H1N1),
35 A/Shangdong/9/93 (H3N2), and B/Panama/45/90 influenza strains. Both the recombinant rHAO and

Table 5: Comparison of trivalent rHAO vaccine with Fluvirin®.

<u>GMT (n=10 mice)</u> <u>Virus strain</u> <u>used as antigen</u>	Trivalent rHAO Influenza vaccine		Fluvirin® GMT (n=10 mice)	
	<u>anti-HA IgG</u>		<u>anti-HA IgG</u>	
	<u>week 0</u>	<u>week 3</u>	<u>week 0</u>	<u>week 3</u>
A/Texas/36/91 (H1N1)	<1000	103,000	<1000	11,200
A/Shangdong/32/92 (H3N2)	<1000	162,400	<1000	41,000
B/Panama/45/90	<1000	164,800	<1000	26,000
<u>Virus strain</u> <u>used as antigen</u>	<u>HAI</u>		<u>HAI</u>	
A/Texas/36/91 (H1N1)	<8	1,522	<8	1,088
A/Shangdong/32/92 (H3N2)	<8	494	<8	435
B/Panama/45/90	<8	174	<8	42
<u>Virus strain</u> <u>used as antigen</u>	<u>Neutralizing Ab</u>		<u>Neutralizing Ab</u>	
A/Texas/36/91 (H1N1)	<100	5,800	<100	2,720
A/Shangdong/32/92 (H3N2)	<100	840	<100	360
B/Panama/45/90	<100	1,300	<100	700

Modifications and variations of the methods and compositions described herein for use in preparing and using a recombinant influenza vaccine will be obvious to those skilled in the art. Such modifications and variations are intended to come within the scope of the appended claims.

67

SEQUENCE LISTING

- (1) GENERAL INFORMATION:
- (i) APPLICANT: MicroGeneSys, Inc.
 - (ii) TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA HEMAGGLUTININ MULTIVALENT VACCINES
 - (iii) NUMBER OF SEQUENCES: 32
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Patrea L. Pabst
 - (B) STREET: 2800 One Atlantic Center
1201 West Peachtree Street
 - (C) CITY: Atlanta
 - (D) STATE: GA
 - (E) COUNTRY: USA
 - (F) ZIP: 30309-3450
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US95/06750
 - (B) FILING DATE: 26-MAY-1995
 - (C) CLASSIFICATION:
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (404)-873-8794
 - (B) TELEFAX: (404)-873-8795
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Influenza virus
 - (x) PUBLICATION INFORMATION:
 - (A) AUTHORS: Davis, et al.
 - (B) TITLE: Construction and Characterization of a Bacterial Clone Containing the Hemagglutinin Gene of the WSN Strain (HON1) of Influenza Virus
 - (C) JOURNAL: Gene
 - (D) VOLUME: 10
 - (F) PAGES: 205-218
 - (G) DATE: 1980
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCAAAAGCA GG

12

- (2) INFORMATION FOR SEQ ID NO:2:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGGGGTACCC CCGGGAGCAA AAGCAGGGGA AAATAAAAA

39

- (2) INFORMATION FOR SEQ ID NO:3:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

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- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCGGTACCT CAKATKCATA TTCTGCACTG CAAAG

35

- (2) INFORMATION FOR SEQ ID NO:4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGGGTACCC CCGGGGACAC AATATGTATA GGCTACCAT

39

- (2) INFORMATION FOR SEQ ID NO:5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCGGTACCT CAKATKCATA TTCTGCACTG CAAAG

35

- (2) INFORMATION FOR SEQ ID NO:6:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1793 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Influenza virus
 - (C) INDIVIDUAL ISOLATE: A/Beijing/32/92 rHA
 - (ix) FEATURE
 - (A) NAME/KEY: polyhedrin mRNA leader (partial)
 - (B) LOCATION: 1 to 18
 - (ix) FEATURE
 - (A) NAME/KEY: coding region for AcNPV 61K protein signal sequence
 - (B) LOCATION: 19 to 72
 - (ix) FEATURE
 - (A) NAME/KEY: SmaI restriction site
 - (B) LOCATION: 76 to 81
 - (ix) FEATURE
 - (A) NAME/KEY: coding region for mature rHA
 - (B) LOCATION: 73 to 1728
 - (ix) FEATURE
 - (A) NAME/KEY: KpnI restriction site
 - (B) LOCATION: 1771 to 1777
 - (ix) FEATURE
 - (A) NAME/KEY: BglII restriction site
 - (B) LOCATION: 1776 to 1782
 - (ix) FEATURE
 - (A) NAME/KEY: universal translation termination signal
 - (B) LOCATION: 1783 to 1793
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TAAAAAACC TATAAATAAT GCCCTTGTAC AAATTGTAA ACGTTTTGTG GTTGGTCGCC

60

GTTTCTAACG CGATTCCCGG GGAATTTCCA GGAAATGACA ACAGCACAGC AACGCTGTGC

120

CTGGGACATC	ATGCAGTGCC	AAACGGAACG	CTAGTGAAAA	CAATCACGAA	TGATCAAATT	180
GAAGTGACTA	ATGCTACTGA	GCTGGTTCAG	AGTTCCTCAA	CAGGTAGAAT	ATGCGACAGT	240
CCTCACCGAA	TCCTTGATGG	AAAAAAGTGC	ACACTGATAG	ATGCTCTATT	GGGAGACCCT	300
CATTGTGATG	GCTTCCAAAA	TAAGGAATGG	GACCTTTTGG	TTGAACGCAG	CAAAGCTTAC	360
AGCAACTGTT	ACCCTTATGA	TGTACCGGAT	TATGCCTCCC	TTAGGTCACT	AGTTGCCTCA	420
TCAGGCACCC	TGGAGTTTAT	CAATGAAGAC	TTCAATTGGA	CTGGAGTCGC	TCAGGATGGG	480
GGAAGCTATG	CTTGCAAAAG	GGGATCTGTT	AACAGTTTCT	TTAGTAGATT	GAATTGGTTG	540
CACAAATCAG	AATACAAATA	TCCAGCGCTG	AACGTGACTA	TGCCAAACAA	TGGCAAATTT	600
GACAAATTGT	ACATTTGGGG	GGTTCACCAC	CCGAGCACGG	ACAGAGACCA	AACCAGCCTA	660
TATGTTGAG	CATCAGGGAG	AGTCACAGTC	TCTACCAAAA	GAAGCCAACA	AACTGTAACC	720
CCGAATATCG	GGTCTAGACC	CTGGGTAAGG	GGTCAGTCCA	GTAAGAATAAG	CATCTATTGG	780
ACAATAGTAA	AACCGGGAGA	CATACTTTTG	ATTAATAGCA	CAGGGAATCT	AATTGCTCCT	840
CGGGGTTACT	TCAAAATACG	AAATGGGAAA	AGCTCAATAA	TGAGGTCAGA	TGCACCCATT	900
GGCACCTGCA	GTTCTGAATG	CATCACTCCA	AATGGAAGCA	TTCCCAATGA	CAAACCTTTT	960
CAAAATGTAA	ACAGGATCAC	ATATGGGGCC	TGCCCCAGAT	ATGTTAAGCA	AAACACTCTG	1020
AAATTGGCAA	CAGGGATGCG	GAATGTACCA	GAGAAACAAA	CTAGAGGCAT	ATTGCGCGCA	1080
ATCGCAGGTT	TCATAGAAAA	TGTTTGGGAG	GGAATGGTAG	ACGGTTGGTA	CGGTTTCAGG	1140
CATCAAAATT	CTGAGGGCAC	AGGACAAGCA	GCAGATCTTA	AAAGCACTCA	AGCAGCAATC	1200
GACCAAATCA	ACGGGAAACT	GAATAGGTTA	ATCGAGAAAA	CGAACGAGAA	ATTCCATCAA	1260
ATCGAAAAAG	AATTCTCAGA	AGTAGAAGGG	AGAATTCAGG	ACCTCGAGAA	ATATGTTGAA	1320
GACACTAAAA	TAGATCTCTG	GTCTTACAAC	GCGGAGCTTC	TTGTTGCCCT	GGAGAACCAC	1380
CATACAATTG	ATCTAACTGA	CTCAGAAATG	AACAACTGT	TTGAAAAAAC	AAGGAAGCAA	1440
CTGAGGGAAA	ATGCTGAGGA	CATGGGCAAT	GGTTGCTTCA	AAATATACCA	CAAATGTGAC	1500
AATGCCTGCA	TAGGGTCAAT	CAGAAATGGA	ACTTATGACC	ATGATGTATA	CAGAGACGAA	1560
GCATTAAACA	ACCGGTTCCA	GATCAAAGGT	GTTGAGCTGA	AGTCAGGATA	CAAAGATTGG	1620
ATCCTATGGA	TTTCCTTTGC	CATATCATGC	TTTTTGCTTT	GTGTGTTTTT	GCTGGGGTTC	1680
ATCATGTGGG	CCTGCCAAAA	AGGCAACATT	AGGTGCAACA	TTGCATTG	AGTGATTATA	1740
TTAAAAACAC	CCTTGTTTCT	AGGATGATTC	GGTACCAGAT	CTTAATTAAT	TAA	1793

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 570 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
 (C) INDIVIDUAL ISOLATE: A/Beijing/32/92 rHA
 (ix) FEATURE
 (A) NAME/KEY: AcNPV 61K protein signal sequence
 (B) LOCATION: 1 to 18
 (ix) FEATURE
 (A) NAME/KEY: mature rHA
 (B) LOCATION: 19 to 552
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

Met Pro Leu Tyr Lys Leu Leu Asn Val Leu Trp Leu Val Ala Val Ser
1      5      10      15
Asn Ala Ile Pro Gly Asp Phe Pro Gly Asn Asp Asn Ser Thr Ala Thr
20      25      30
Leu Cys Leu Gly His His Ala Val Pro Asn Gly Thr Leu Val Lys Thr
35      40      45
Ile Thr Asn Asp Gln Ile Glu Val Thr Asn Ala Thr Glu Leu Val Gln
50      55      60
Ser Ser Ser Thr Gly Arg Ile Cys Asp Ser Pro His Arg Ile Leu Asp
65      70      75      80
Gly Lys Asn Cys Thr Leu Ile Asp Ala Leu Leu Gly Asp Pro His Cys
85      90      95
Asp Gly Phe Gln Asn Lys Glu Trp Asp Leu Phe Val Glu Arg Ser Lys
100     105     110
Ala Tyr Ser Asn Cys Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu
115     120     125
Arg Ser Leu Val Ala Ser Ser Gly Thr Leu Glu Phe Ile Asn Glu Asp
130     135     140
Phe Asn Trp Thr Gly Val Ala Gln Asp Gly Gly Ser Tyr Ala Cys Lys
145     150     155     160
Arg Gly Ser Val Asn Ser Phe Phe Ser Arg Leu Asn Trp Leu His Lys
165     170     175
Ser Glu Tyr Lys Tyr Pro Ala Leu Asn Val Thr Met Pro Asn Asn Gly
180     185     190
Lys Phe Asp Lys Leu Tyr Ile Trp Gly Val His His Pro Ser Thr Asp
195     200     205
Arg Asp Gln Thr Ser Leu Tyr Val Arg Ala Ser Gly Arg Val Thr Val
210     215     220
Ser Thr Lys Arg Ser Gln Gln Thr Val Thr Pro Asn Ile Gly Ser Arg
225     230     235     240
Pro Trp Val Arg Gly Gln Ser Ser Arg Ile Ser Ile Tyr Trp Thr Ile
245     250     255
Val Lys Pro Gly Asp Ile Leu Leu Ile Asn Ser Thr Gly Asn Leu Ile
260     265     270
Ala Pro Arg Gly Tyr Phe Lys Ile Arg Asn Gly Lys Ser Ser Ile Met
275     280     285
Arg Ser Asp Ala Pro Ile Gly Thr Cys Ser Ser Glu Cys Ile Thr Pro
290     295     300
Asn Gly Ser Ile Pro Asn Asp Lys Pro Phe Gln Asn Val Asn Arg Ile
305     310     315     320
Thr Tyr Gly Ala Cys Pro Arg Tyr Val Lys Gln Asn Thr Leu Lys Leu
325     330     335
Ala Thr Gly Met Arg Asn Val Pro Glu Lys Gln Thr Arg Gly Ile Phe
340     345     350
Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu Gly Met Val Asp
355     360     365
Gly Trp Tyr Gly Phe Arg His Gln Asn Ser Glu Gly Thr Gly Gln Ala
370     375     380

Ala Asp Leu Lys Ser Thr Gln Ala Ala Ile Asp Gln Ile Asn Gly Lys
385     390     395     400
Leu Asn Arg Leu Ile Glu Lys Thr Asn Glu Lys Phe His Gln Ile Glu
405     410     415
Lys Glu Phe Ser Glu Val Glu Gly Arg Ile Gln Asp Leu Glu Lys Tyr
420     425     430
Val Glu Asp Thr Lys Ile Asp Leu Trp Ser Tyr Asn Ala Glu Leu Leu
435     440     445

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71

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Val Ala Leu Glu Asn Gln His Thr Ile Asp Leu Thr Asp Ser Glu Met
  450                      455                      460
Asn Lys Leu Phe Glu Lys Thr Arg Lys Gln Leu Arg Glu Asn Ala Glu
  465                      470                      475                      480
Asp Met Gly Asn Gly Cys Phe Lys Ile Tyr His Lys Cys Asp Asn Ala
                      485                      490                      495
Cys Ile Gly Ser Ile Arg Asn Gly Thr Tyr Asp His Asp Val Tyr Arg
      500                      505                      510
Asp Glu Ala Leu Asn Asn Arg Phe Gln Ile Lys Gly Val Glu Leu Lys
      515                      520                      525
Ser Gly Tyr Lys Asp Trp Ile Leu Trp Ile Ser Phe Ala Ile Ser Cys
      530                      535                      540
Phe Leu Leu Cys Val Val Leu Leu Gly Phe Ile Met Trp Ala Cys Gln
      545                      550                      555                      560
Lys Gly Asn Ile Arg Cys Asn Ile Cys Ile
                      565                      570

```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (C) INDIVIDUAL ISOLATE: A/Texas/36/91 rHA

(ix) FEATURE

- (A) NAME/KEY: polyhedrin mRNA leader (partial)
- (B) LOCATION: 1 to 18

(ix) FEATURE

- (A) NAME/KEY: coding region for AcNPV 61K protein signal peptide
- (B) LOCATION: 19 to 72

(ix) FEATURE

- (A) NAME/KEY: SmaI restriction site
- (B) LOCATION: 76 to 81

(ix) FEATURE

- (A) NAME/KEY: KpnI restriction site
- (B) LOCATION: 82 to 87

(ix) FEATURE

- (A) NAME/KEY: SmaI restriction site
- (B) LOCATION: 88 to 93

(ix) FEATURE

- (A) NAME/KEY: coding region for mature rHA
- (B) LOCATION: 73 to 1734

(ix) FEATURE

- (A) NAME/KEY: KpnI restriction site
- (B) LOCATION: 1744 to 1749

(ix) FEATURE

- (A) NAME/KEY: BglII restriction site
- (B) LOCATION: 1750 to 1755

(ix) FEATURE

- (A) NAME/KEY: universal translation termination signal
- (B) LOCATION: 1756 to 1766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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TAAAAAACC TATAAATAAT GCCCTTGTAC AAATTGTTAA ACGTTTTGTG GTTGGTCGCC      60
GTTTCTAACG CGATTCCCGG GGGTACCCCC GGGGACACAA TATGTATAGG CTACCATGCG      120
AACAACTCAA CCGACACTGT TGACACAGTA CTTGAGAAGA ACGTGACAGT GACACACTCT      180
GTCAACCTAC TTGAGGACAG TCACAACGGA AAATATGTC GACTAAAGGG AATAGCCCCA      240

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CTACAATTGG GTAATTGCAG CGTTGCCGGA TGGATCTTAG GAAACCCAAA ATGCGAATCA 300
CTGTTTTCTA AGGAATCATG GTCCTACATT GCAGAAACAC CAAACCCTGA GAATGGAACA 360
TGTTACCCAG GGTATTTTCG CGACTATGAG GAACTGAGGG AGCAATTGAG TTCAGTATCA 420
TCATTGAGAG GATTGGAAT ATTCCCCAAA GAAAGCTCAT GGCCCAACCA CACCGTAACC 480
AAAGGAGTAA CGAGATCATG CTCCCATAAT GGGAAAAGCA GTTTTACAG AAATTTGCTA 540
TGGCTGACGG AGAAGAATGG CTTGTACCCA AATCTGAGCA AGTCCTATGT AAACAACAAA 600
GAGAAAGAAG TCCTTGTAAT ATGGGGTGTT CATCACCCGT CTAACATAAG GGACCAAAGG 660
GCCATCTATC ATACAGAAAA TGCTTATGTC TCTGTAGTGT CTTACATTA TAGCAGAAGA 720
TTCACCCAG AAATAGCAAA AAGACCCAAA GTAAGAGATC AAGAAGGAAG AATTAACACT 780
TACTGGACTC TGCTGGAACC CGGGGACACA ATAATATTG AGGCAAATGG AAATCTAATA 840
GCGCCATGGT ATGCTTTTCG ACTGAGTAGA GGCTTTGGGT CAGGAATCAT CACCTCAAAC 900
GCATCAATGG ATGAATGTGA CGCGAAGTGT CAAACACCCC AGGGAGCTAT AACAGTAGT 960
CTTCCTTTCC AGAATGTACA CCCAGTCACA ATAGGAGAGT GTCCAAAGTA TGTCAGGAGT 1020
ACAAAATTAA GGATGGTTAC AGGACTAAGG AACATCCCAT CCATTCAATC CAGAGGTTTG 1080
TTTGAGGCCA TTGCCGTTT CATTGAAGGG GGGTGGACTG GAATGATAGA TGGATGGTAT 1140
GGTTATCATC ATCAGAATGA ACAAGGATCT GGCTATGCTG CGGACCAAAA AAGCACACAA 1200
AATGCCATTA ACGGGATTAC AAACAAGGTG AATTCTGTAA TCGAGAAAAT GAACACTCAA 1260
TTCACAGCTG TGGGCAAAGA ATTCAACAAA TTAGAAAGAA GGATGGAAAA CTTAAATAAA 1320
AAAGTTGATG ATGGATTCT GGACATTGG ACATATAATG CAGAATTGTT GGTCTACTG 1380
GAAAATGGAA GGACTTTGGA TTTTCATGAC TCAAATGTGA AGAATCTGTA TGAGAAAGTA 1440
AAAAGCCAAT TGAAGAATAA TGCCAAAGAA ATAGGGAACG GGTGTTTTGA ATTCTATCAC 1500
AAGTGTAACA ATGAATGCAT GGAAAGTGTG AAAAATGGAA CTTATGACTA TCCAAAATAT 1560
TCCGAAGAAT CAAAGTTAAA CAGGGGAAAA ATTGATGGAG TGAAATTGGA ATCAATGGGA 1620
GTCTATCAGA TTCTGGCGAT CTA CTCAACT GTCGCCAGT CACTGGTGCT TTTGGTCTCC 1680
CTGGGGGCAA TCAGCTTCTG GATGTGTTCT AATGGGTCTT TGCAGTGCAG AATATGAATC 1740
TGAGGTACCA GATCTTAAT AATTAA 1766

```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (C) INDIVIDUAL ISOLATE: A/Texas/36/91 rHA

(ix) FEATURE

- (A) NAME/KEY: AcNPV 61K protein signal sequence

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(B) LOCATION: 1 to 18

(ix) FEATURE

(A) NAME/KEY: mature rHA

(B) LOCATION: 19 to 554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

Met Pro Leu Tyr Lys Leu Leu Asn Val Leu Trp Leu Val Ala Val Ser
1      5      10      15
Asn Ala Ile Pro Gly Gly Thr Pro Gly Asp Thr Ile Cys Ile Gly Tyr
20      25      30
His Ala Asn Asn Ser Thr Asp Thr Val Asp Thr Val Leu Glu Lys Asn
35      40      45
Val Thr Val Thr His Ser Val Asn Leu Leu Glu Asp Ser His Asn Gly
50      55      60
Lys Leu Cys Arg Leu Lys Gly Ile Ala Pro Leu Gln Leu Gly Asn Cys
65      70      75      80
Ser Val Ala Gly Trp Ile Leu Gly Asn Pro Lys Cys Glu Ser Leu Phe
85      90      95
Ser Lys Glu Ser Trp Ser Tyr Ile Ala Glu Thr Pro Asn Pro Glu Asn
100     105     110
Gly Thr Cys Tyr Pro Gly Tyr Phe Ala Asp Tyr Glu Glu Leu Arg Glu
115     120     125
Gln Leu Ser Ser Val Ser Ser Phe Glu Arg Phe Glu Ile Phe Pro Lys
130     135     140
Glu Ser Ser Trp Pro Asn His Thr Val Thr Lys Gly Val Thr Arg Ser
145     150     155     160
Cys Ser His Asn Gly Lys Ser Ser Phe Tyr Arg Asn Leu Leu Trp Leu
165     170     175
Thr Glu Lys Asn Gly Leu Tyr Pro Asn Leu Ser Lys Ser Tyr Val Asn
180     185     190
Asn Lys Glu Lys Glu Val Leu Val Leu Trp Gly Val His His Pro Ser
195     200     205
Asn Ile Arg Asp Gln Arg Ala Ile Tyr His Thr Glu Asn Ala Tyr Val
210     215     220
Ser Val Val Ser Ser His Tyr Ser Arg Arg Phe Thr Pro Glu Ile Ala
225     230     235     240
Lys Arg Pro Lys Val Arg Asp Gln Glu Gly Arg Ile Asn Tyr Tyr Trp
245     250     255
Thr Leu Leu Glu Pro Gly Asp Thr Ile Ile Phe Glu Ala Asn Gly Asn
260     265     270
Leu Ile Ala Pro Trp Tyr Ala Phe Ala Leu Ser Arg Gly Phe Gly Ser
275     280     285
Gly Ile Ile Thr Ser Asn Ala Ser Met Asp Glu Cys Asp Ala Lys Cys
290     295     300
Gln Thr Pro Gln Gly Ala Ile Asn Ser Ser Leu Pro Phe Gln Asn Val
305     310     315     320
His Pro Val Thr Ile Gly Glu Cys Pro Lys Tyr Val Arg Ser Thr Lys
325     330     335
Leu Arg Met Val Thr Gly Leu Arg Asn Ile Pro Ser Ile Gln Ser Arg
340     345     350
Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Gly Gly Trp Thr Gly
355     360     365
Met Ile Asp Gly Trp Tyr Gly Tyr His His Gln Asn Glu Gln Gly Ser
370     375     380
Gly Tyr Ala Ala Asp Gln Lys Ser Thr Gln Asn Ala Ile Asn Gly Ile
385     390     395     400
Thr Asn Lys Val Asn Ser Val Ile Glu Lys Met Asn Thr Gln Phe Thr
405     410     415

Ala Val Gly Lys Glu Phe Asn Lys Leu Glu Arg Arg Met Glu Asn Leu
420     425     430
Asn Lys Lys Val Asp Asp Gly Phe Leu Asp Ile Trp Thr Tyr Asn Ala
435     440     445
Glu Leu Val Leu Leu Glu Asn Gly Arg Thr Leu Asp Phe His Asp
450     455     460
Ser Asn Val Lys Asn Leu Tyr Glu Lys Val Lys Ser Gln Leu Lys Asn
465     470     475     480

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74

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Asn Ala Lys Glu Ile Gly Asn Gly Cys Phe Glu Phe Tyr His Lys Cys
      485                               490           495
Asn Asn Glu Cys Met Glu Ser Val Lys Asn Gly Thr Tyr Asp Tyr Pro
      500                               505           510
Lys Tyr Ser Glu Glu Ser Lys Leu Asn Arg Gly Lys Ile Asp Gly Val
      515                               520           525
Lys Leu Glu Ser Met Gly Val Tyr Gln Ile Leu Ala Ile Tyr Ser Thr
      530                               535           540
Val Ala Ser Ser Leu Val Leu Leu Val Ser Leu Gly Ala Ile Ser Phe
      545                               555           560
Trp Met Cys Ser Asn Gly Ser Leu Gln Cys Arg Ile
      565                               570

```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (C) INDIVIDUAL ISOLATE: B/Panama/45/90 rHA

(ix) FEATURE

- (A) NAME/KEY: polyhedrin mRNA leader (partial)
- (B) LOCATION: 1 to 18

(ix) FEATURE

- (A) NAME/KEY: coding region for HA signal peptide sequence
- (B) LOCATION: 19 to 69

(ix) FEATURE

- (A) NAME/KEY: SmaI restriction site
- (B) LOCATION: 22 to 27

(ix) FEATURE

- (A) NAME/KEY: coding region for mature rHA
- (B) LOCATION: 70 to 1773

(ix) FEATURE

- (A) NAME/KEY: KpnI restriction site
- (B) LOCATION: 1777 to 1782

(ix) FEATURE

- (A) NAME/KEY: BglII restriction site
- (B) LOCATION: 1783 to 1788

(ix) FEATURE

- (A) NAME/KEY: universal translation termination signal
- (B) LOCATION: 1789 to 1799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

TAAAAAACC TATAATAAT GCCCCGGAAG GCAATAATTG TACTACTCAT GGTAGTAACA      60
TCCAACGCAG ATCGAATCTG CACTGGGATA ACATCTTCAA ACTCACCTCA TGTGGTCAAA      120
ACAGCTACTC AAGGGGAAGT CAATGTGACT GGTGTGATAC CACTGACAAC AACACCAACA      180
AAATCTCATT TTGCAAATCT AAAAGGAACA AAGACCAGAG GGAAACTATG CCCAAACTGT      240
CTCAACTGCA CAGATCTGGA TGTGGCCTTG GGCAGACCAA TGTGTGTGGG GACCACACCT      300
TCGGCAAAAG CTTCAATACT CCACGAAGTC AGACCTGTTA CATCCGGGTG CTTTCCTATA      360
ATGCACGACA GAACAAAAAT CAGACAGCTA CCAATCTTC TCAGAGGATA TGAAAATATC      420
AGATTATCAA CCCAAAACGT TATCAACGCA GAAAGAGCAC CAGGAGGACC CTACAGACTT      480
GGAACCTCAG GATCTTGCCC TAACGTTACC AGTAGAGACG GATTCTTCGC AACAATGGCT      540

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RECTIFIED SHEET (RULE 91)
ISA/EP

TGGGCTGTCC CAAGGGACAA CAAAACAGCA ACGAATCCAC TAACAGTAGA AGTACCATAC 600
 ATTTGTACCA AAGGAGAAGA CCAAATTACT GTTTGGGGGT TCCATTCTGA TAACAAAATC 660
 CAAATGAAAA ACCTCTATGG AGACTCAAAT CCTCAAAAGT TCACCTCATC TGCCAATGGA 720
 GTAACCAACAC ATTATGTTTC TCAGATTGGT GGCTTCCCAA ATCAAACAGA AGACGGAGGG 780
 CTACCACAAA GCGGCAGAAT TGTTGTTGAT TACATGGTGC AAAAACCTGG GAAAACAGGA 840
 ACAATTGTCT ATCAAAGAGG TGTTTTGTTG CCTCAAAAGG TGTGGTGCGC AAGTGGCAGG 900
 AGCAAGGTAA TAAAAGGGTC CTTGCCTTTA ATTGGTGAAG CAGATTGCCT TCACGAAAAA 960
 TACGGTGGAT TAAACAAAAG CAAGCCTTAC TACACAGGAG AACATGCAA AGCCATAGGA 1020
 AATTGCCCAA TATGGGTGAA AACACCTTTG AAGCTTGCCA ATGGAACCAA ATATAGACCT 1080
 CCTGCAAAAC TATTAAAGGA AAGGGGTTTC TTCGAGCTA TTGCTGGTTT CTTAGAAGGA 1140
 GGATGGGAAG GAATGATTGC AGGTTGGCAC GGATACACAT CTCATGGAGC ACATGGAGTG 1200
 GCAGTGGCAG CAGACCTTAA GAGTACGCAA GAAGCCATAA ACAAGATAAC AAAAAATCTC 1260
 AATTCCTTTGA GTGAGCTAGA AGTAAAGAAT CTTCAAAGAC TAAGTGGTGC CATGGATGAA 1320
 CTCCACAACG AAATACTCGA GCTGGATGAG AAAGTGGATG ATCTCAGAGC TGACACAATA 1380
 AGCTCGCAA TAGAGCTTGC AGTCTTGCTT TCCAACGAAG GAATAATAAA CAGTGAAGAT 1440
 GAGCATCTAT TGGCACTTGA GAGAAACTA AAGAAATGC TGGGTCCCTC TGCTGTAGAC 1500
 ATAGGGAATG GATGCTTCGA AACCAAACAC AAGTGCAACC AGACCTGCTT AGACAGGATA 1560
 GCTGCTGGCA CCTTTAATGC AGGAGAATTT TCTCTCCCA CTTTGTATC ACTGAATATT 1620
 ACTGCTGCAT CTTTAAATGA TGATGGATTG GATAATCATA CTATACTGCT CTACTACTCA 1680
 ACTGCTGCTT CTAGTTTGGC TGTAACATTG ATGATAGCTA TTTTATTGT TTATATGGTC 1740
 TCCAGAGACA ATGTTTCTTG TTCCATCTGT CTGTGAGGTA CCAGATCTTA ATTAATTAA 1799

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 585 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Influenza virus
 - (C) INDIVIDUAL ISOLATE: B/Panama/45/90 rHA
- (ix) FEATURE
 - (A) NAME/KEY: HA signal peptide
 - (B) LOCATION: 1 to 17
- (ix) FEATURE
 - (A) NAME/KEY: mature rHA
 - (B) LOCATION: 18 to 568
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Pro Gly Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asn
 1 5 10 15
 Ala Asp Arg Ile Cys Thr Gly Ile Thr Ser Ser Asn Ser Pro His Val
 20 25 30

Val Lys Thr Ala Thr Gln Gly Glu Val Asn Val Thr Gly Val Ile Pro
 35 40 45
 Leu Thr Thr Thr Pro Thr Lys Ser His Phe Ala Asn Leu Lys Gly Thr
 50 55 60
 Lys Thr Arg Gly Lys Leu Cys Pro Asn Cys Leu Asn Cys Thr Asp Leu
 65 70 75 80
 Asp Val Ala Leu Gly Arg Pro Met Cys Val Gly Thr Thr Pro Ser Ala
 85 90 95
 Lys Ala Ser Ile Leu His Glu Val Arg Pro Val Thr Ser Gly Cys Phe
 100 105 110
 Pro Ile Met His Asp Arg Thr Lys Ile Arg Gln Leu Pro Asn Leu Leu
 115 120 125
 Arg Gly Tyr Glu Asn Ile Arg Leu Ser Thr Gln Asn Val Ile Asn Ala
 130 135 140
 Glu Arg Ala Pro Gly Gly Pro Tyr Arg Leu Gly Thr Ser Gly Ser Cys
 145 150 155 160
 Pro Asn Val Thr Ser Arg Asp Gly Phe Phe Ala Thr Met Ala Trp Ala
 165 170 175
 Val Pro Arg Asp Asn Lys Thr Ala Thr Asn Pro Leu Thr Val Glu Val
 180 185 190
 Pro Tyr Ile Cys Thr Lys Gly Glu Asp Gln Ile Thr Val Trp Gly Phe
 195 200 205
 His Ser Asp Asn Lys Ile Gln Met Lys Asn Leu Tyr Gly Asp Ser Asn
 210 215 220
 Pro Gln Lys Phe Thr Ser Ser Ala Asn Gly Val Thr Thr His Tyr Val
 225 230 235 240
 Ser Gln Ile Gly Gly Phe Pro Asn Gln Thr Glu Asp Gly Gly Leu Pro
 245 250 255
 Gln Ser Gly Arg Ile Val Val Asp Tyr Met Val Gln Lys Pro Gly Lys
 260 265 270
 Thr Gly Thr Ile Val Tyr Gln Arg Gly Val Leu Leu Pro Gln Lys Val
 275 280 285
 Trp Cys Ala Ser Gly Arg Ser Lys Val Ile Lys Gly Ser Leu Pro Leu
 290 295 300
 Ile Gly Glu Ala Asp Cys Leu His Glu Lys Tyr Gly Gly Leu Asn Lys
 305 310 315 320
 Ser Lys Pro Tyr Tyr Thr Gly Glu His Ala Lys Ala Ile Gly Asn Cys
 325 330 335
 Pro Ile Trp Val Lys Thr Pro Leu Lys Leu Ala Asn Gly Thr Lys Tyr
 340 345 350
 Arg Pro Pro Ala Lys Leu Leu Lys Glu Arg Gly Phe Phe Gly Ala Ile
 355 360 365
 Ala Gly Phe Leu Glu Gly Gly Trp Glu Gly Met Ile Ala Gly Trp His
 370 375 380
 Gly Tyr Thr Ser His Gly Ala His Gly Val Ala Val Ala Asp Leu
 385 390 395 400
 Lys Ser Thr Gln Glu Ala Ile Asn Lys Ile Thr Lys Asn Leu Asn Ser
 405 410 415
 Leu Ser Glu Leu Glu Val Lys Asn Leu Gln Arg Leu Ser Gly Ala Met
 420 425 430
 Asp Glu Leu His Asn Glu Ile Leu Glu Leu Asp Glu Lys Val Asp Asp
 435 440 445
 Leu Arg Ala Asp Thr Ile Ser Ser Gln Ile Glu Leu Ala Val Leu Leu
 450 455 460
 Ser Asn Glu Gly Ile Ile Asn Ser Glu Asp Glu His Leu Leu Ala Leu
 465 470 475 480
 Glu Arg Lys Leu Lys Lys Met Leu Gly Pro Ser Ala Val Asp Ile Gly
 485 490 495

 Asn Gly Cys Phe Glu Thr Lys His Lys Cys Asn Gln Thr Cys Leu Asp
 500 505 510
 Arg Ile Ala Ala Gly Thr Phe Asn Ala Gly Glu Phe Ser Leu Pro Thr
 515 520 525
 Phe Asp Ser Leu Asn Ile Thr Ala Ala Ser Leu Asn Asp Asp Gly Leu
 530 535 540
 Asp Asn His Thr Ile Leu Leu Tyr Tyr Ser Thr Ala Ala Ser Ser Leu
 545 550 555 560

Ala Val Thr Leu Met Ile Ala Ile Phe Ile Val Tyr Met Val Ser Arg
565 570 575
Asp Asn Val Ser Cys Ser Ile Cys Leu
580 585

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Influenza virus

(C) INDIVIDUAL ISOLATE: B/Netherlands/13/94 rHA

(ix) **FEATURE**

- (A) NAME/KEY: polyhedrin mRNA leader (partial)
(B) LOCATION: 1 to 18

(1x) FEATURE

- (A) NAME/KEY: coding region for AcNPV 61K protein signal
sequence
- (B) LOCATION: 19 to 72

(ix) FEATURE

- (A) NAME/KEY: SmaI restriction site
(B) LOCATION: 76 to 81

(ix) **FEATURE**

- (A) NAME/KEY: coding region for mature rHA
(B) LOCATION: 73 to 1785

(ix) **FEATURE**

- (A) NAME/KEY: KpnI restriction site
(B) LOCATION: 1789 to 1794

(ix) **FEATURE**

- (A) NAME/KEY: BglII restriction site
(B) LOCATION: 1795 to 1800

(ix) **FEATURE**

- (A) NAME/KEY: universal translation termination signal
(B) LOCATION: 1801 to 1811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TAAAAAAACC	TATAAATAAT	GCCCTTGATC	AAATTGTTAA	ACGTTTGTG	GTTGGTCGCC	60
GTTTCTAACG	CGATTCCCGG	GGATCGAATC	TGCACTGGGA	TAACATCTTC	AAAATCACCT	120
CATGTAGTCA	AAACAGCTAC	TCAAGGGGAG	GTCAATGTGA	CTGGTGTGAT	ACCACTGACG	180
ACAACACCAA	CAAAATCTCA	TTTTGCAAAT	CTCAAAGGAA	CAAAGACCAG	AGGGAAACTA	240
TGCCCAAAC	GTCTCAACTG	CACAGATCTG	GATGTGGCCT	TGGGCAGACC	AATGTGTGTG	300
GGGATCACAC	CTTCGGCAAA	AGCTTCAATA	CTCCACGAAG	TCAGACCTGT	TACATCCGGG	360
TGCTTTCCTA	TAATGCATGA	CAGAACAAAA	ATCAGACAGC	TACCCAATCT	TCTCAGAGGA	420
TATGAAAACA	TCAGACTATC	AACCCAAAA	GTTATCAACG	CAGAAAAGGC	ACCAGGAGGA	480
CCCTACAGAC	TTGGAACCTC	AGGATCTTGC	CCTAACGTTA	CCAGTAGAAC	CGGATTCTTC	540
GCAACAATGG	CTTGGGCTGT	CCCAAGGGAC	AACAAAACAG	CAACGAATCC	ACTAACAGTA	600
GAAGTACCAT	ACATTTGTAC	GAAAGGAGAA	GACCAAATTA	CTGTTTGGGG	GTTCCATTCT	660
GATAACAAAA	CCCAAATGAA	AAACCTCTAT	GGAGACTCAA	ATCCTCAAAA	GTTACCTCA	720
TCTGCCAATG	GAGTAACCA	ACATTATGTT	TCTCAGATTG	GTGGCTTCCC	AGATCAACA	780

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GAAGACGGAG GACTACCACA AAGCGGCAGA ATTGTTGTTG ATTACATGGT GCAAAAACCT      840
GGGAAAACAG GAACAATTGT CTATCAAAGA GGTATTTTGT TGCCTCAAAA GGTGTGGTGC      900
GCAAGTGGCA GGAGCAAGGT AATAAAAGGG TCCTTGCCTT TAATTGGTGA AGCAGATTGC      960
CTTCACGAAA AATACGGTGG ATTAAACAAA AGCAAGCCTT ACTACACAGG AGAACATGCA     1020
AAAGCCATAG GAAATTGCCC AATATGGGTG AAAACACCTT TGAAGCTTGC CAATGGAACC     1080
AGATATAGAC CTCCTGCAAA ACTATTAAAG GAAAGGGGTT TCTTCGGAGC TATTGCTGGT     1140
TTCTTAGAAG GAGGATGGGA AGGAATGATT GCAGGTTGGC ACGGATACAC ATCTCACGGG     1200
GCACATGGAG TGGCAGTGGC AGCAGACCTT AAGAGTACGC AAGAAGCCAT AAACAAGATA     1260
ACAAAAAATC TCAATTCTTT GAGTGAGCTA GAAGTAAAGA ACCTTCAAAG ACTAAGTGGT     1320
GCCATGGATG AACTCCACAA CGAAATACTC GAGCTGGATG AGAAAGTGA TGATCTCAGA     1380
GCTGACACAA TAAGCTCGCA AATAGAGCTT GCAGTCTTAC TTTCCAACGA AGGAATAATA     1440
AACAGTGAAG ATGAGCATCT ATTGGCACTT GAGAGAAAAC TAAAGAAAAT GCTGGGTCCC     1500
TCTGCTGTAG ACATAGGGAA TGGATGCTTC GAAACAAAAC ACAAGTGCAA CCAGACCTGC     1560
TTAGACAGGA TAGCTGCTGG CACCTTTAAT GCAGGAGAAT TTTCTCTTCC CACTTTTGAT     1620
TCACTGAATA TTAGTGCTGC ATCTTTAAAT GATGATGGAT TGGATAATCA TACTATACTG     1680
CTCTACTACT CAACTGCTGC TTCTAGTTTG GCTGTAACAT TGATGATAGC TATTTTTATT     1740
GTTTATATGG TCTCCAGAGA CAATGTTTCT TGTTCCATCT GTCTGTGAGG TACCAGATCT     1800
TAATTAATTA A                                                    1811

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (C) INDIVIDUAL ISOLATE: B/Netherlands/13/94 rHA

(ix) FEATURE

- (A) NAME/KEY: AcNPV 61K protein signal sequence
- (B) LOCATION: 1 to 18

(ix) FEATURE

- (A) NAME/KEY: mature rHA
- (B) LOCATION: 19 to 571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Met Pro Leu Tyr Lys Leu Leu Asn Val Leu Trp Leu Val Ala Val Ser
1          5          10          15
Asn Ala Ile Pro Gly Asp Arg Ile Cys Thr Gly Ile Thr Ser Ser Lys
          20          25          30
Ser Pro His Val Val Lys Thr Ala Thr Gln Gly Glu Val Asn Val Thr
          35          40          45
Gly Val Ile Pro Leu Thr Thr Pro Thr Lys Ser His Phe Ala Asn
          50          55          60
Leu Lys Gly Thr Lys Thr Arg Gly Lys Leu Cys Pro Asn Cys Leu Asn
65          70          75          80

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Cys Thr Asp Leu Asp Val Ala Leu Gly Arg Pro Met Cys Val Gly Ile
 85 90 95
 Thr Pro Ser Ala Lys Ala Ser Ile Leu His Glu Val Arg Pro Val Thr
 100 105 110
 Ser Gly Cys Phe Pro Ile Met His Asp Arg Thr Lys Ile Arg Gln Leu
 115 120 125
 Pro Asn Leu Leu Arg Gly Tyr Glu Asn Ile Arg Leu Ser Thr Gln Asn
 130 135 140
 Val Ile Asn Ala Glu Lys Ala Pro Gly Gly Pro Tyr Arg Leu Gly Thr
 145 150 155 160
 Ser Gly Ser Cys Pro Asn Val Thr Ser Arg Thr Gly Phe Phe Ala Thr
 165 170 175
 Met Ala Trp Ala Val Pro Arg Asp Asn Lys Thr Ala Thr Asn Pro Leu
 180 185 190
 Thr Val Glu Val Pro Tyr Ile Cys Thr Lys Gly Glu Asp Gln Ile Thr
 195 200 205
 Val Trp Gly Phe His Ser Asp Asn Lys Thr Gln Met Lys Asn Leu Tyr
 210 215 220
 Gly Asp Ser Asn Pro Gln Lys Phe Thr Ser Ser Ala Asn Gly Val Thr
 225 230 235 240
 Thr His Tyr Val Ser Gln Ile Gly Gly Phe Pro Asp Gln Thr Glu Asp
 245 250 255
 Gly Gly Leu Pro Gln Ser Gly Arg Ile Val Val Asp Tyr Met Val Gln
 260 265 270
 Lys Pro Gly Lys Thr Gly Thr Ile Val Tyr Gln Arg Gly Ile Leu Leu
 275 280 285
 Pro Gln Lys Val Trp Cys Ala Ser Gly Arg Ser Lys Val Ile Lys Gly
 290 295 300
 Ser Leu Pro Leu Ile Gly Glu Ala Asp Cys Leu His Glu Lys Tyr Gly
 305 310 315 320
 Gly Leu Asn Lys Ser Lys Pro Tyr Tyr Thr Gly Glu His Ala Lys Ala
 325 330 335
 Ile Gly Asn Cys Pro Ile Trp Val Lys Thr Pro Leu Lys Leu Ala Asn
 340 345 350
 Gly Thr Arg Tyr Arg Pro Pro Ala Lys Leu Leu Lys Glu Arg Gly Phe
 355 360 365
 Phe Gly Ala Ile Ala Gly Phe Leu Glu Gly Gly Trp Glu Gly Met Ile
 370 375 380
 Ala Gly Trp His Gly Tyr Thr Ser His Gly Ala His Gly Val Ala Val
 385 390 395 400
 Ala Ala Asp Leu Lys Ser Thr Gln Glu Ala Ile Asn Lys Ile Thr Lys
 405 410 415
 Asn Leu Asn Ser Leu Ser Glu Leu Glu Val Lys Asn Leu Gln Arg Leu
 420 425 430
 Ser Gly Ala Met Asp Glu Leu His Asn Glu Ile Leu Glu Leu Asp Glu
 435 440 445
 Lys Val Asp Asp Leu Arg Ala Asp Thr Ile Ser Ser Gln Ile Glu Leu
 450 455 460
 Ala Val Leu Leu Ser Asn Glu Gly Ile Ile Asn Ser Glu Asp Glu His
 465 470 475 480
 Leu Leu Ala Leu Glu Arg Lys Leu Lys Lys Met Leu Gly Pro Ser Ala
 485 490 495
 Val Asp Ile Gly Asn Gly Cys Phe Glu Thr Lys His Lys Cys Asn Gln
 500 505 510
 Thr Cys Leu Asp Arg Ile Ala Ala Gly Thr Phe Asn Ala Gly Glu Phe
 515 520 525
 Ser Leu Pro Thr Phe Asp Ser Leu Asn Ile Thr Ala Ala Ser Leu Asn
 530 535 540
 Asp Asp Gly Leu Asp Asn His Thr Ile Leu Leu Tyr Tyr Ser Thr Ala
 545 550 555 560
 Ala Ser Ser Leu Ala Val Thr Leu Met Ile Ala Ile Phe Ile Val Tyr
 565 570 575
 Met Val Ser Arg Asp Asn Val Ser Cys Ser Ile Cys Leu
 580 585

(2) INFORMATION FOR SEQ ID NO:14:

RECTIFIED SHEET (RULE 91)
ISA/EP

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1757 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Influenza virus
 - (C) INDIVIDUAL ISOLATE: A/Shandong/9/93 rHA
- (ix) FEATURE
 - (A) NAME/KEY: polyhedrin mRNA leader (partial)
 - (B) LOCATION: 1 to 18
- (ix) FEATURE
 - (A) NAME/KEY: coding region for AcNPV 61K protein signal sequence
 - (B) LOCATION: 19 to 72
- (ix) FEATURE
 - (A) NAME/KEY: SmaI restriction site
 - (B) LOCATION: 76 to 81
- (ix) FEATURE
 - (A) NAME/KEY: coding region for mature rHA
 - (B) LOCATION: 73 to 1728
- (ix) FEATURE
 - (A) NAME/KEY: KpnI restriction site
 - (B) LOCATION: 1735 to 1740
- (ix) FEATURE
 - (A) NAME/KEY: BglII restriction site
 - (B) LOCATION: 1741 to 1746
- (ix) FEATURE
 - (A) NAME/KEY: universal translation termination signal
 - (B) LOCATION: 1747 to 1757
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

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TAAAAAACC TATAATAAT GCCCTGTAC AAATTGTTAA ACGTTTGTG GTTGGTCGCC      60
GTTTCTAACG CGATTCCCGG GCAAGACCTT CCAGGAAATG ACAACAGCAC AGCAACGCTG    120
TGCCTGGGAC ATCATGCAGT GCCAAACGGA ACGCTAGTGA AAACAATCAC GAATGATCAA    180
ATTGAAGTGA CTAATGCTAC TGAGTTGGTT CAGAGTTCCT CAACAGGTAG AATATGCGGC    240
AGTCCTCACC GAATCCTTGA TGGAAAAAC TGCACACTGA TAGATGCTCT ATTGGGAGAC    300
CCTCATTGTG ATGGCTTCCA AAATAAGGAA TGGGACCTTT TTGTTGAACG CAGCAAAGCT    360
TACAGCAACT GTTACCCTTA TGATGTGCCG GATTATGCCT CCCTTAGGTC ACTAGTTGCC    420
TCATCAGGCA CCCTGGAGTT TATCAATGAA GACTTCAATT GGA CTGGAGT CGCTCAGGAT    480
GGGGGAAGCT ATGCTTGCAA AAGAGGATCT GTTAACAGTT TCTTTAGTAG ATTGAATTGG    540
TTGCACAAAT TAGAATACAA ATATCCAGCG CTGAACGTGA CTATGCCAAA CAATGGCAAA    600
TTTGACAAAT TGTACATTTG GGGGGTTCAC CACCCGAGCA CGGACAGTGA CCAAACCAGC    660
CTATATGTTT GAGCATCAGG GAGAGTCACA GTCTCTACCA AAAGAAGCCA ACAAACGTGA    720
ACCCCGAATA TCGGGTCTAG ACCCTGGGTA AGGGGTCAGT CCAGTAGAAT AAGCATCTAT    780
TGGACAATAG TAAAACCGGG AGACATACTT TTGATTGATA GCACAGGGAA TCTAATTGCT    840
CCTCGGGGTT ACTTCAAAAT ACGAAATGGG AAAAGCTCAA TAATGAGGTC AGATGCACCC    900
ATTGGCAACT GCAGTTCTGA ATGCATCACT CCAAATGGAA GCATTCCCAA TGACAAACCT    960

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TTTCAAAATG TAAACAGAAT CACATATGGG GCCTGCCCCA GATATGTTAA GCAAAACACT 1020
CTGAAATTGG CAACAGGGAT GCGGAATGTA CCAGAGAAAC AAAC TAGAGG CATATTCGGC 1080
GCAATCGCAG GTTTCATAGA AAATGGTTGG GAGGGAATGG TAGACGGTTG GTACGGTTTC 1140
AGGCATCAAA ATTCTGAGGG CACAGGACAA GCAGCAGATC TTAAGACAC TCAAGCAGCA 1200
ATCGACCAAA TCAACGGGAA ACTGAATAGG TTAATCGAGA AAACGAACGA GAAATTCAT 1260
CAAATCGAAA AAGAATTCTC AGAAGTAGAA GGGAGAATTC AGGACCTCGA GAAATATGTT 1320
GAAGACACTA AAATAGATCT CTGGTCTTAC AACGCGGAGC TTCTTGTTGC CCTGGAGAAC 1380
CAACATACAA TTGATCTAAC TGAATCAGAA ATGAACAAAC TGTGTTGAAA AACAAGGAAG 1440
CAACTGAGGG AAAATGCTGA GGACATGGGC AATGGTTGCT TCAAAATATA CCACAAATGT 1500
GACAATGCCT GCATAGGGTC AATCAGAAAT GGAAC TTATG ACCATGATGT ATACAGAGAC 1560
GAAGCATTAA ACAACCGGTT CCAGATCAAA GGTGTTGAGC TGAAGTCAGG ATACAAAGAT 1620
TGGATCCTAT GGATTTCCTT TGCCATATCA TGCTTTTTC TTTGTGTTGT TTTGCTGGGG 1680
TTCATCATGT GGGCTGCCA AAAAGGCAAC ATTAGGTGCA ACATTTGCAT TTGAGGTACC 1740
AGATCTTAAT TAATTAA 1757

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(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 571 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Influenza virus
 - (C) INDIVIDUAL ISOLATE: A/Shandong/9/93 rHA
- (ix) FEATURE
 - (A) NAME/KEY: AcNPV 61K protein signal sequence
 - (B) LOCATION: 1 to 18
- (ix) FEATURE
 - (A) NAME/KEY: mature rHA
 - (B) LOCATION: 19 to 553
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

Met Pro Leu Tyr Lys Leu Leu Asn Val Leu Trp Leu Val Ala Val Ser
1      5      10      15
Asn Ala Ile Pro Gly Gln Asp Leu Pro Gly Asn Asp Asn Ser Thr Ala
20     25     30
Thr Leu Cys Leu Gly His His Ala Val Pro Asn Gly Thr Leu Val Lys
35     40     45
Thr Ile Thr Asn Asp Gln Ile Glu Val Thr Asn Ala Thr Glu Leu Val
50     55     60
Gln Ser Ser Ser Thr Gly Arg Ile Cys Gly Ser Pro His Arg Ile Leu
65     70     75     80
Asp Gly Lys Asn Cys Thr Leu Ile Asp Ala Leu Leu Gly Asp Pro His
85     90     95
Cys Asp Gly Phe Gln Asn Lys Glu Trp Asp Leu Phe Val Glu Arg Ser
100    105    110
Lys Ala Tyr Ser Asn Cys Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
115    120    125
Leu Arg Ser Leu Val Ala Ser Ser Gly Thr Leu Glu Phe Ile Asn Glu
130    135    140

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Asp Phe Asn Trp Thr Gly Val Ala Gln Asp Gly Gly Ser Tyr Ala Cys
145      150      155      160
Lys Arg Gly Ser Val Asn Ser Phe Phe Ser Arg Leu Asn Trp Leu His
      165      170      175
Lys Leu Glu Tyr Lys Tyr Pro Ala Leu Asn Val Thr Met Pro Asn Asn
      180      185      190
Gly Lys Phe Asp Lys Leu Tyr Ile Trp Gly Val His His Pro Ser Thr
      195      200      205
Asp Ser Asp Gln Thr Ser Leu Tyr Val Arg Ala Ser Gly Arg Val Thr
      210      215      220
Val Ser Thr Lys Arg Ser Gln Gln Thr Val Thr Pro Asn Ile Gly Ser
      225      230      235      240
Arg Pro Trp Val Arg Gly Gln Ser Ser Arg Ile Ser Ile Tyr Trp Thr
      245      250      255
Ile Val Lys Pro Gly Asp Ile Leu Leu Ile Asp Ser Thr Gly Asn Leu
      260      265      270
Ile Ala Pro Arg Gly Tyr Phe Lys Ile Arg Asn Gly Lys Ser Ser Ile
      275      280      285
Met Arg Ser Asp Ala Pro Ile Gly Asn Cys Ser Ser Glu Cys Ile Thr
      290      295      300
Pro Asn Gly Ser Ile Pro Asn Asp Lys Pro Phe Gln Asn Val Asn Arg
      305      310      315      320
Ile Thr Tyr Gly Ala Cys Pro Arg Tyr Val Lys Gln Asn Thr Leu Lys
      325      330      335
Leu Ala Thr Gly Met Arg Asn Val Pro Glu Lys Gln Thr Arg Gly Ile
      340      345      350
Phe Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu Gly Met Val
      355      360      365
Asp Gly Trp Tyr Gly Phe Arg His Gln Asn Ser Glu Gly Thr Gly Gln
      370      375      380
Ala Ala Asp Leu Lys Ser Thr Gln Ala Ala Ile Asp Gln Ile Asn Gly
      385      390      395      400
Lys Leu Asn Arg Leu Ile Glu Lys Thr Asn Glu Lys Phe His Gln Ile
      405      410      415
Glu Lys Glu Phe Ser Glu Val Glu Gly Arg Ile Gln Asp Leu Glu Lys
      420      425      430
Tyr Val Glu Asp Thr Lys Ile Asp Leu Trp Ser Tyr Asn Ala Glu Leu
      435      440      445
Leu Val Ala Leu Glu Asn Gln His Thr Ile Asp Leu Thr Asp Ser Glu
      450      455      460
Met Asn Lys Leu Phe Glu Lys Thr Arg Lys Gln Leu Arg Glu Asn Ala
      465      470      475      480
Glu Asp Met Gly Asn Gly Cys Phe Lys Ile Tyr His Lys Cys Asp Asn
      485      490      495
Ala Cys Ile Gly Ser Ile Arg Asn Gly Thr Tyr Asp His Asp Val Tyr
      500      505      510
Arg Asp Glu Ala Leu Asn Asn Arg Phe Gln Ile Lys Gly Val Glu Leu
      515      520      525
Lys Ser Gly Tyr Lys Asp Trp Ile Leu Trp Ile Ser Phe Ala Ile Ser
      530      535      540
Cys Phe Leu Leu Cys Val Val Leu Leu Gly Phe Ile Met Trp Ala Cys
      545      550      555      560
Gln Lys Gly Asn Ile Arg Cys Asn Ile Cys Ile
      565      570

```

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1814 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Influenza virus
 - (C) INDIVIDUAL ISOLATE: B/Shanghai/4/94 rHA

- (ix) FEATURE
 (A) NAME/KEY: polyhedrin mRNA leader (partial)
 (B) LOCATION: 1 to 18
- (ix) FEATURE
 (A) NAME/KEY: coding region for AcNPV 61K protein signal sequence
 (B) LOCATION: 19 to 72
- (ix) FEATURE
 (A) NAME/KEY: SmaI restriction site
 (B) LOCATION: 76 to 81
- (ix) FEATURE
 (A) NAME/KEY: KpnI restriction site
 (B) LOCATION: 82 to 87
- (ix) FEATURE
 (A) NAME/KEY: coding region for mature rHA
 (B) LOCATION: 73 to 1794
- (ix) FEATURE
 (A) NAME/KEY: universal translation termination signal
 (B) LOCATION: 1804 to 1814
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TAAAAAACC TATAATAAT GCCCTTGAC AAATTGTAA ACGTTTTGTG GTTGGTCGCC	60
GTTTCTAAG CGATTCCCGG GGGTACCGAT CGAATCTGCA CTGGGATAAC ATCTTCAAAC	120
TCACCTCATG TGGTCAAAAC AGCTACTCAA GGGGAGGTCA ATGTGACTGG TGTGATACCA	180
GTGACAACAA CACCAACAAA ATCTCATTTT GCAAATCTCA AAGGAACAAA GACCAGAGGG	240
AAACTATGCC CAACTGTCT CAACTGCACA GATCTGGATG TGGCCTTGGG CAGACCAATG	300
TGTGTGGGGA CCACACCTTC GGCAAAAGCT TCAATACTCC ACGAAGTCAG ACCTGTTACA	360
TCCGGGTGCT TTCCTATAAT GCACGACAGA ACAAATCA GACAGCTACC CAATCTTCTC	420
AGAGGATATG AAAATATCAG ATTATCAACC CAAACGTTA TCAACGCAGA AAAGGCACCA	480
GGAGGACCCT ACAGACTTGG AACCTCAGGA TCTTGCCCTA ACGCTACCAG TAGAAGCGGA	540
TTTTTCGCAA CAATGGCTTG GGCTGTCCCA AGGGACAACA ACAAACAGC AACGAATCCA	600
CTAACAGTAG AAGTACCATA CATTTGCACA AAAGGAGAAG ACCAAATTAC TGTTTGGGGG	660
TTCCATTCTG ATAACAAACC CCAAATGAAA AACCTCTATG GAGACTCAA TCCTCAAAG	720
TTCACTCAT CTGCTAATGG AGTAACCACA CATTATGTTT CTCAGATTGG CGGCTTCCCA	780
GATCAAACAG AAGACGGAGG GCTACCACAA AGCGGCAGAA TTGTTGTTGA TTACATGGTG	840
CAAAACCTG GGAAGACAGG AACAATTGTC TATCAGAGAG GTGTTTTGTT GCCTCAAAG	900
GTGTGGTGCG CTAGTGGCAG GAGCAAAGTA ATAAAGGGT CCTTGCCTTT AATTGGTGAA	960
GCAGATTGCC TTCACGAAAA ATACGGTGGA TTAACAAAA GCAAGCCTTA CTACACAGGA	1020
GAACATGCAA AAGCCATAGG AAATTGCCCA ATATGGGTGA AAACACCTTT GAAGCTTGCC	1080
AATGGAACCA AATATAGACC TCCTGCAAAA CTATTAAAGG AAAGGGGTTT CTTCGGAGCT	1140
ATTGCTGGTT TCTTAGAAGG AGGATGGGAA GGAATGATTG CAGGTTGGCA CGGATACACA	1200
TCTCACGGAG CACATGGAGT GGCAGTGGCA GCAGACCTTA AGAGTACGCA AGAAGCCATA	1260
AACAAGATAA CAAAAATCT CAATTCTTTG AGTGAGCTAG AAGTAAAGAA TCTTCAAAGG	1320
CTAAGTGGTG CCATGGATGA ACTCCACAAC GAAATACTCG AGCTGGATGA GAAAGTGGAT	1380

GATCTCAGAG CTGACACAAT AAGCTCGCAA ATAGAACTTG CAGTCTTGCT TTCCAACGAA 1440
 GGAATAATAA ACAGTGAAGA TGAGCATCTA TTGGCACTTG AGAGAAAAC T AAAGAAAATG 1500
 CTGGGTCCCT CTGCTGTAGA CATAGGAAAT GGATGCTTCG AAACCAAACA CAAGTGCAAC 1560
 CAGACCTGCT TAGACAGGAT AGCTGCTGGC ACCTTTAATG CGGGAGAATT TTCTCTTCCC 1620
 ACTTTTGATT CACTGAATAT TACTGCTGCA TCTTTAAATG ATGATGGATT GGATAACCAT 1680
 ACTATACTGC TCTACTACTC AACTGCTGCT TCTAGTTTGG CGGTAACATT GATGATAGCT 1740
 ATTTTATTG TTTATATGGT CTCCAGAGAC AATGTTTCTT GCTCCATCTG TCTGTGAGGA 1800
 TCTTAATTAA TTAA 1814

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (C) INDIVIDUAL ISOLATE: B/Shanghai/4/94 rHA

(ix) FEATURE

- (A) NAME/KEY: AcNPV 61K protein signal peptide
- (B) LOCATION: 1 to 18

(ix) FEATURE

- (A) NAME/KEY: mature rHA
- (B) LOCATION: 19 to 574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Pro Leu Tyr Lys Leu Leu Asn Val Leu Trp Leu Val Ala Val Ser
 1 5 10 15
 Asn Ala Ile Pro Gly Gly Thr Asp Arg Ile Cys Thr Gly Ile Thr Ser
 20 25 30
 Ser Asn Ser Pro His Val Val Lys Thr Ala Thr Gln Gly Glu Val Asn
 35 40 45
 Val Thr Gly Val Ile Pro Leu Thr Thr Thr Pro Thr Lys Ser His Phe
 50 55 60
 Ala Asn Leu Lys Gly Thr Lys Thr Arg Gly Lys Leu Cys Pro Asn Cys
 65 70 75 80
 Leu Asn Cys Thr Asp Leu Asp Val Ala Leu Gly Arg Pro Met Cys Val
 85 90 95
 Gly Thr Thr Pro Ser Ala Lys Ala Ser Ile Leu His Glu Val Arg Pro
 100 105 110
 Val Thr Ser Gly Cys Phe Pro Ile Met His Asp Arg Thr Lys Ile Arg
 115 120 125
 Gln Leu Pro Asn Leu Leu Arg Gly Tyr Glu Asn Ile Arg Leu Ser Thr
 130 135 140
 Gln Asn Val Ile Asn Ala Glu Lys Ala Pro Gly Gly Pro Tyr Arg Leu
 145 150 155 160
 Gly Thr Ser Gly Ser Cys Pro Asn Ala Thr Ser Arg Ser Gly Phe Phe
 165 170 175
 Ala Thr Met Ala Trp Ala Val Pro Arg Asp Asn Asn Lys Thr Ala Thr
 180 185 190
 Asn Pro Leu Thr Val Glu Val Pro Tyr Ile Cys Thr Lys Gly Glu Asp
 195 200 205
 Gln Ile Thr Val Trp Gly Phe His Ser Asp Asn Lys Pro Gln Met Lys
 210 215 220
 Asn Leu Tyr Gly Asp Ser Asn Pro Gln Lys Phe Thr Ser Ser Ala Asn
 225 230 235 240

85

Gly Val Thr Thr His Tyr Val Ser Gln Ile Gly Gly Phe Pro Asp Gln
 245 250 255
 Thr Glu Asp Gly Gly Leu Pro Gln Ser Gly Arg Ile Val Val Asp Tyr
 260 265 270
 Met Val Gln Lys Pro Gly Lys Thr Gly Thr Ile Val Tyr Gln Arg Gly
 275 280 285
 Val Leu Leu Pro Gln Lys Val Trp Cys Ala Ser Gly Arg Ser Lys Val
 290 295 300
 Ile Lys Gly Ser Leu Pro Leu Ile Gly Glu Ala Asp Cys Leu His Glu
 305 310 315 320
 Lys Tyr Gly Gly Leu Asn Lys Ser Lys Pro Tyr Tyr Thr Gly Glu His
 325 330 335
 Ala Lys Ala Ile Gly Asn Cys Pro Ile Trp Val Lys Thr Pro Leu Lys
 340 345 350
 Leu Ala Asn Gly Thr Lys Tyr Arg Pro Pro Ala Lys Leu Lys Glu
 355 360 365
 Arg Gly Phe Phe Gly Ala Ile Ala Gly Phe Leu Glu Gly Gly Trp Glu
 370 375 380
 Gly Met Ile Ala Gly Trp His Gly Tyr Thr Ser His Gly Ala His Gly
 385 390 395 400
 Val Ala Val Ala Ala Asp Leu Lys Ser Thr Gln Glu Ala Ile Asn Lys
 405 410 415
 Ile Thr Lys Asn Leu Asn Ser Leu Ser Glu Leu Glu Val Lys Asn Leu
 420 425 430
 Gln Arg Leu Ser Gly Ala Met Asp Glu Leu His Asn Glu Ile Leu Glu
 435 440 445
 Leu Asp Glu Lys Val Asp Asp Leu Arg Ala Asp Thr Ile Ser Ser Gln
 450 455 460
 Ile Glu Leu Ala Val Leu Leu Ser Asn Glu Gly Ile Ile Asn Ser Glu
 465 470 475 480
 Asp Glu His Leu Leu Ala Leu Glu Arg Lys Leu Lys Lys Met Leu Gly
 485 490 495
 Pro Ser Ala Val Asp Ile Gly Asn Gly Cys Phe Glu Thr Lys His Lys
 500 505 510
 Cys Asn Gln Thr Cys Leu Asp Arg Ile Ala Ala Gly Thr Phe Asn Ala
 515 520 525
 Gly Glu Phe Ser Leu Pro Thr Phe Asp Ser Leu Asn Ile Thr Ala Ala
 530 535 540
 Ser Leu Asn Asp Asp Gly Leu Asp Asn His Thr Ile Leu Leu Tyr Tyr
 545 550 555 560
 Ser Thr Ala Ala Ser Ser Leu Ala Val Thr Leu Met Ile Ala Ile Phe
 565 570 575
 Ile Val Tyr Met Val Ser Arg Asp Asn Val Ser Cys Ser Ile Cys Leu
 580 585 590

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (C) INDIVIDUAL ISOLATE: B/Harbin/7/94 rHA

(ix) FEATURE

- (A) NAME/KEY: polyhedrin mRNA leader (partial)
- (B) LOCATION: 1 to 18

(ix) FEATURE

- (A) NAME/KEY: coding region for HA signal peptide sequence
- (B) LOCATION: 19 to 69

(ix) FEATURE

- (A) NAME/KEY: SmaI restriction site
- (B) LOCATION: 22 to 27

- (ix) FEATURE
 (A) NAME/KEY: coding region for mature rHA
 (B) LOCATION: 70 to 1776
- (ix) FEATURE
 (A) NAME/KEY: KpnI restriction site
 (B) LOCATION: 1780 to 1785
- (ix) FEATURE
 (A) NAME/KEY: BglII restriction site
 (B) LOCATION: 1786 to 1791
- (ix) FEATURE
 (A) NAME/KEY: universal translation termination signal
 (B) LOCATION: 1792 to 1802
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TAAAAAAACC TATAAATAAT GCCCGGAAG GCAATAATTG TACTACTCAT GGTAGTAACA	60
TCCAACGCAG ATCGAATCTG CACTGGGATA ACATCTTCAA ACTCACCTCA TGTGGTCAAA	120
ACAGCTACTC AAGGGGAAGT CAATGTGACT GGTGTGATAC CACTGACAAC AACACCAACA	180
AAATCTCATT TTGCAATCT AAAAGGAACA AAGACCAGAG GGAACTATG CCCAACTGT	240
CTCAACTGCA CAGATCTGGA TGTGGCCTTG GGCAGACCAA TGTGTGTGGG GACCACACCT	300
TCGGCAAAAG CTTCAATACT CCACGAAGTC AGACCTGTTA CATCCGGGTG CTTTCCTATA	360
ATGCACGACA GAACAAAAT CAGACAGCTA CCCAATCTTC TCAGAGGATA TGAAAATATC	420
AGATTATCAA CCCAAAACGT TATCAATGCA GAAAAGCAC CAGGAGGACC CTACAGACTT	480
GGAACCTCAG GATCTTGCCC TAACGCTACC AGTAGAAGCG GATTTTTTGC AACAAATGGCT	540
TGGGCTGTCC CAAGGGACGA CAACAAAACA GCAACGAATC CACTAACAGT AGAAGTACCA	600
TACGTTTGTA CAGAAGGAGA AGACCAAATT ACTGTTTGGG GGTTCATTC TGATAACAAA	660
GCCCAAATGA AAAACCTCTA TGGAGACTCA AATCCTCAA AGTTCACCTC ATCTGCTAAT	720
GGAGTAACCA CACATTATGT TTCTCAGATT GCGGGCTTCC CAGATCAAAC AGAAGACGGA	780
GGGCTACCAC AAAGCGGCAG AATTGTTGTT GATTACATGG TGCAAAAACC TGGGAAAACA	840
GGAACAATTG TCTATCAAAG AGGTGTTTTG TTGCCTCAA AGGTGTGGTG CGCGAGTGGC	900
AGGAGCAAAG TAATAAAAGG GTCCTTGCCT TTAATTGGTG AAGCAGATTG CCTTCACGAA	960
AAATACGGTG GATTAAACAA AAGCAAGCCT TACTACACAG GAGAACATGC AAAAGCCATA	1020
GGAAATTGCC CAATATGGGT GAAAACACCT TTGAAGCTTG CCAATGGAAC CAAATATAGA	1080
CCTCCTGCAA AACTATTAAA GGAAAGGGGT TTCTTCGGAG CTATTGCTGG TTTCTTAGAA	1140
GGAGGATGGG AAGGAATGAT TGCAGGTTGG CACGGATACA CATCTCACGG AGCACATGGA	1200
GTGGCAGTGG CAGCAGACCT TAAGAGTACG CAAGAAGCCA TAAACAAGAT AACAAAAAAT	1260
CTCAATTCTT TGAGTGAGCT AGAAGTAAAG AATCTTCAA GACTAAGTGG TGCCATGGAT	1320
GAAGCTCCATA ACGAAATACT CGAGCTGGAT GAGAAAGTGG ATGATCTCAG AGCTGACACT	1380
ATAAGCTCGC AAATAGAACT TGCAGTCTTG CTTTCCAACG AAGGAATAAT AAACAGTGAA	1440
GATGAGCATC TATTGGCACT TGAGAGAAAA CTAAAGAAAA TGCTGGGTCC CTCTGCTGTA	1500
GACATAGGGA ATGGATGCTT CGAAACCAAA CACAAGTGCA ACCAGACCTG CTTAGACAGG	1560
ATAGCTGCTG GCACCTTTAA TGCAGGAGAA TTTTCTCTCC CCACTTTTGA TTTACTGAAT	1620

ATTACTGCTG CATCTTTAAA TGATGATGGA TTGGATAATC ATACTATACT GCTCTACTAC 1680
 TCAACTGCTG CTTCTAGTTT GGCTGTAACA TTGATGATAG CTATTTTAT TGTATTATG 1740
 GTCTCCAGAG ACAATGTTTC ATGCTCCATC TGTCTGTGAG GTACCAGATC TTAATTAATT 1800
 AA 1802

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (C) INDIVIDUAL ISOLATE: B/Harbin/7/94 rHA

(ix) FEATURE

- (A) NAME/KEY: HA signal peptide
- (B) LOCATION: 1 to 17

(ix) FEATURE

- (A) NAME/KEY: mature rHA
- (B) LOCATION: 18 to 569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Pro Gly Lys Ala Ile Ile Val Leu Leu Met Val Val Thr Ser Asn
 1 5 10 15
 Ala Asp Arg Ile Cys Thr Gly Ile Thr Ser Ser Asn Ser Pro His Val
 20 25 30
 Val Lys Thr Ala Thr Gln Gly Glu Val Asn Val Thr Gly Val Ile Pro
 35 40 45
 Leu Thr Thr Thr Pro Thr Lys Ser His Phe Ala Asn Leu Lys Gly Thr
 50 55 60
 Lys Thr Arg Gly Lys Leu Cys Pro Asn Cys Leu Asn Cys Thr Asp Leu
 65 70 75 80
 Asp Val Ala Leu Gly Arg Pro Met Cys Val Gly Thr Thr Pro Ser Ala
 85 90 95
 Lys Ala Ser Ile Leu His Glu Val Arg Pro Val Thr Ser Gly Cys Phe
 100 105 110
 Pro Ile Met His Asp Arg Thr Lys Ile Arg Gln Leu Pro Asn Leu Leu
 115 120 125
 Arg Gly Tyr Glu Asn Ile Arg Leu Ser Thr Gln Asn Val Ile Asn Ala
 130 135 140
 Glu Lys Ala Pro Gly Gly Pro Tyr Arg Leu Gly Thr Ser Gly Ser Cys
 145 150 155 160
 Pro Asn Ala Thr Ser Arg Ser Gly Phe Phe Ala Thr Met Ala Trp Ala
 165 170 175
 Val Pro Arg Asp Asp Asn Lys Thr Ala Thr Asn Pro Leu Thr Val Glu
 180 185 190
 Val Pro Tyr Val Cys Thr Glu Gly Glu Asp Gln Ile Thr Val Trp Gly
 195 200 205
 Phe His Ser Asp Asn Lys Ala Gln Met Lys Asn Leu Tyr Gly Asp Ser
 210 215 220
 Asn Pro Gln Lys Phe Thr Ser Ser Ala Asn Gly Val Thr Thr His Tyr
 225 230 235 240
 Val Ser Gln Ile Gly Gly Phe Pro Asp Gln Thr Glu Asp Gly Gly Leu
 245 250 255
 Pro Gln Ser Gly Arg Ile Val Val Asp Tyr Met Val Gln Lys Pro Gly
 260 265 270
 Lys Thr Gly Thr Ile Val Tyr Gln Arg Gly Val Leu Leu Pro Gln Lys
 275 280 285
 Val Trp Cys Ala Ser Gly Arg Ser Lys Val Ile Lys Gly Ser Leu Pro
 290 295 300

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Leu Ile Gly Glu Ala Asp Cys Leu His Glu Lys Tyr Gly Gly Leu Asn
305                      310                      315                      320
Lys Ser Lys Pro Tyr Tyr Thr Gly Glu His Ala Lys Ala Ile Gly Asn
                      325                      330                      335
Cys Pro Ile Trp Val Lys Thr Pro Leu Lys Leu Ala Asn Gly Thr Lys
                      340                      345                      350
Tyr Arg Pro Pro Ala Lys Leu Leu Lys Glu Arg Gly Phe Phe Gly Ala
                      355                      360                      365
Ile Ala Gly Phe Leu Glu Gly Gly Trp Glu Gly Met Ile Ala Gly Trp
                      370                      375                      380
His Gly Tyr Thr Ser His Gly Ala His Gly Val Ala Val Ala Ala Asp
385                      390                      395                      400
Leu Lys Ser Thr Gln Glu Ala Ile Asn Lys Ile Thr Lys Asn Leu Asn
                      405                      410                      415
Ser Leu Ser Glu Leu Glu Val Lys Asn Leu Gln Arg Leu Ser Gly Ala
                      420                      425                      430
Met Asp Glu Leu His Asn Glu Ile Leu Glu Leu Asp Glu Lys Val Asp
                      435                      440                      445
Asp Leu Arg Ala Asp Thr Ile Ser Ser Gln Ile Glu Leu Ala Val Leu
                      450                      455                      460
Leu Ser Asn Glu Gly Ile Ile Asn Ser Glu Asp Glu His Leu Leu Ala
465                      470                      475                      480
Leu Glu Arg Lys Leu Lys Lys Met Leu Gly Pro Ser Ala Val Asp Ile
                      485                      490                      495
Gly Asn Gly Cys Phe Glu Thr Lys His Lys Cys Asn Gln Thr Cys Leu
                      500                      505                      510
Asp Arg Ile Ala Ala Gly Thr Phe Asn Ala Gly Glu Phe Ser Leu Pro
                      515                      520                      525
Thr Phe Asp Ser Leu Asn Ile Thr Ala Ala Ser Leu Asn Asp Asp Gly
                      530                      535                      540
Leu Asp Asn His Thr Ile Leu Leu Tyr Tyr Ser Thr Ala Ala Ser Ser
545                      550                      555                      560
Leu Ala Val Thr Leu Met Ile Ala Ile Phe Ile Val Tyr Met Val Ser
                      565                      570                      575
Arg Asp Asn Val Ser Cys Ser Ile Cys Leu
                      580                      585

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(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1757 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (C) INDIVIDUAL ISOLATE: A/Johannesburg/33/94 rHA

(ix) FEATURE

- (A) NAME/KEY: polyhedrin mRNA leader (partial)
- (B) LOCATION: 1 to 18

(ix) FEATURE

- (A) NAME/KEY: coding region for AcNPV 61K protein signal peptide
- (B) LOCATION: 19 to 72

(ix) FEATURE

- (A) NAME/KEY: SmaI restriction site
- (B) LOCATION: 76 to 81

(ix) FEATURE

- (A) NAME/KEY: coding region for mature rHA
- (B) LOCATION: 73 to 1731

(ix) FEATURE

- (A) NAME/KEY: KpnI restriction site
- (B) LOCATION: 1735 to 1740

(ix) FEATURE

- (A) NAME/KEY: BglII restriction site

- (B) LOCATION: 1741 to 1747
 (ix) FEATURE
 (A) NAME/KEY: universal translation termination signal
 (B) LOCATION: 1747 to 1757
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

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TAAAAAAACC TATAATAAT GCCCTTGTAC AAATTGTTAA ACGTTTTGTG GTTGGTCGCC      60
GTTTCTAACG CGATTCCCGG GCAGGACCTT CCAGGAAATG ACAACAGCAC AGCAACGCTG      120
TGCCTGGGAC ACCATGCAGT GCCAAACGGA ACGCTAGTGA AAACAATCAC GAATGATCAA      180
ATTGAAGTGA CTAATGCTAC TGAGCTGGTT CAGAGTTCCC CAACAGGTAG AATATGCGAC      240
AGTCCTCACC GAATCCTTGA TGGAAAGAAC TGCACACTGA TAGATGCTCT ATTGGGAGAC      300
CCTCATTGTG ATGGCTTCCA AAATAAGGAA TGGGACCTTT TTGTTGAACG CAGCAAAGCT      360
TACAGCAACT GTTACCCTTA TGATGTGCCG GATTATGCCT CCCTTAGGTC ACTAGTTGCC      420
TCATCAGGCA CCCTGGAGTT TATCAACGAA AACTTCAATT GGACTGGAGT CGCTCAGGAT      480
GGGAAAAGCT ATGCTTGCAA AAGGGGATCT GTTAACAGTT TCTTTAGTAG ATTGAATTGG      540
TTGCACAAAT TAGAATACAA ATATCCAGCG CTGAACGTGA CTATGCCAAA CAATGGCAAA      600
TTTGACAAAT TGTACATTG GGGGGTTCAC CACCCGAGCA CGGACAGTGA CCAAACCAGC      660
CTATATGTCC GAGCATCAGG GAGAGTCACA GTCTCTACCA AAAGAAGCCA ACAAACCTGTA      720
ATCCCGGATA TCGGGTATAG ACCATGGGTA AGGGGTCAGT CCAGTAGAAT AGGCATCTAT      780
TGGACAATAG TAAAACCGGG AGACATACTT TTGATTAATA GCACAGGGAA TCTAATTGCT      840
CCTCGGGGTT ACTTCAAAAT ACGAAATGGG AAAAGCTCAA TAATGAGGTC AGATGCACCC      900
ATTGGCAACT GCAGTTCTGA ATGCATCACT CCAATGGGAA GCATTCCCAA TGACAAACCT      960
TTTCAAAATG TAAACAGGAT CACATATGGG GCCTGCCCCA GATATGTTAA GCAAAACACT     1020
CTGAAATTGG CAACAGGGAT GCGGAATGTA CCAGAGAAAC AAAC TAGAGG CATATTGCGC     1080
GCAATCGCAG GTTTCATAGA AAATGGTTGG GAGGGAATGG TAGACGGTTG GTACGGTTTC     1140
AGGCATCAAA ATTCTGAGGG CACAGGACAA GCTGCAGATC TTAAAAGCAC TCAAGCAGCA     1200
ATCGACCAAA TCAACGGGAA ACTGAATAGG TTAGTCGAGA AAACGAACGA GAAATTCCAT     1260
CAAAATCGAAA AAGAATTCTC AGAAGTAGAA GGGAGAATTC AGGACCTCGA GAAATATGTT     1320
GAAGACACTA AAATAGATCT CTGGTCTTAC AATGCGGAGC TTCTTGTGTC TCTGGAGAAC     1380
CAACATACAA TTGATCTAAC TGA CTAGAA ATGAACAAAC TGTTTGAAAG AACAAGGAAG     1440
CAACTGAGGG AAAATGCTGA GGACATGGGC AATGGTTGTT TCAAAATATA CCACAAATGT     1500
GACAATGCCT GCATAGGGTC AATCAGAAAT GGAAC TTATG ACCATGATGT ATACAGAGAC     1560
GAAGCATTAA ACAACCGGTT CCAGATCAAA GGTGTTGAGC TGAAGTCAGG ATACAAAGAT     1620
TGGATTCTAT GGATTTCTTT TGCCATATCA TGCTTTTTCG TTTGTGTTGT TTTGCTTGGG     1680
TTCATCATGT GGGCCTGCCA AAAAGGCAAC ATTAGGTGCA ACATTGTCAT TTGAGGTACC     1740
AGATCTTAAT TAATTAA                                     1757

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(2) INFORMATION FOR SEQ ID NO:21:

RECTIFIED SHEET (RULE 91)
 ISA/EP

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 571 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Influenza virus
 (C) INDIVIDUAL ISOLATE: A/Johannesburg/33/94 rHA
- (ix) FEATURE
 (A) NAME/KEY: AcNPV 61K protein signal sequence
 (B) LOCATION: 1 to 18
- (ix) FEATURE
 (A) NAME/KEY: mature rHA
 (B) LOCATION: 19 to 569
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

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Met Pro Leu Tyr Lys Leu Leu Asn Val Leu Trp Leu Val Ala Val Ser
1          5          10          15
Asn Ala Ile Pro Gly Gln Asp Leu Pro Gly Asn Asp Asn Ser Thr Ala
20          25          30
Thr Leu Cys Leu Gly His His Ala Val Pro Asn Gly Thr Leu Val Lys
35          40          45
Thr Ile Thr Asn Asp Gln Ile Glu Val Thr Asn Ala Thr Glu Leu Val
50          55          60
Gln Ser Ser Pro Thr Gly Arg Ile Cys Asp Ser Pro His Arg Ile Leu
65          70          75          80
Asp Gly Lys Asn Cys Thr Leu Ile Asp Ala Leu Leu Gly Asp Pro His
85          90          95
Cys Asp Gly Phe Gln Asn Lys Glu Trp Asp Leu Phe Val Glu Arg Ser
100         105         110
Lys Ala Tyr Ser Asn Cys Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
115         120         125
Leu Arg Ser Leu Val Ala Ser Ser Gly Thr Leu Glu Phe Ile Asn Glu
130         135         140
Asn Phe Asn Trp Thr Gly Val Ala Gln Asp Gly Lys Ser Tyr Ala Cys
145         150         155         160
Lys Arg Gly Ser Val Asn Ser Phe Phe Ser Arg Leu Asn Trp Leu His
165         170         175
Lys Leu Glu Tyr Lys Tyr Pro Ala Leu Asn Val Thr Met Pro Asn Asn
180         185         190
Gly Lys Phe Asp Lys Leu Tyr Ile Trp Gly Val His His Pro Ser Thr
195         200         205
Asp Ser Asp Gln Thr Ser Leu Tyr Val Arg Ala Ser Gly Arg Val Thr
210         215         220
Val Ser Thr Lys Arg Ser Gln Gln Thr Val Ile Pro Asp Ile Gly Tyr
225         230         235         240
Arg Pro Trp Val Arg Gly Gln Ser Ser Arg Ile Gly Ile Tyr Trp Thr
245         250         255
Ile Val Lys Pro Gly Asp Ile Leu Leu Ile Asn Ser Thr Gly Asn Leu
260         265         270
Ile Ala Pro Arg Gly Tyr Phe Lys Ile Arg Asn Gly Lys Ser Ser Ile
275         280         285
Met Arg Ser Asp Ala Pro Ile Gly Asn Cys Ser Ser Glu Cys Ile Thr
290         295         300
Pro Asn Gly Ser Ile Pro Asn Asp Lys Pro Phe Gln Asn Val Asn Arg
305         310         315         320
Ile Thr Tyr Gly Ala Cys Pro Arg Tyr Val Lys Gln Asn Thr Leu Lys
325         330         335
Leu Ala Thr Gly Met Arg Asn Val Pro Glu Lys Gln Thr Arg Gly Ile
340         345         350
Phe Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu Gly Met Val
355         360         365

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91

Asp Gly Trp Tyr Gly Phe Arg His Gln Asn Ser Glu Gly Thr Gly Gln
 370 375 380
 Ala Ala Asp Leu Lys Ser Thr Gln Ala Ala Ile Asp Gln Ile Asn Gly
 385 390 395 400
 Lys Leu Asn Arg Leu Val Glu Lys Thr Asn Glu Lys Phe His Gln Ile
 405 410 415
 Glu Lys Glu Phe Ser Glu Val Glu Gly Arg Ile Gln Asp Leu Glu Lys
 420 425 430
 Tyr Val Glu Asp Thr Lys Ile Asp Leu Trp Ser Tyr Asn Ala Glu Leu
 435 440 445
 Leu Val Ala Leu Glu Asn Gln His Thr Ile Asp Leu Thr Asp Ser Glu
 450 455 460
 Met Asn Lys Leu Phe Glu Arg Thr Arg Lys Gln Leu Arg Glu Asn Ala
 465 470 475 480
 Glu Asp Met Gly Asn Gly Cys Phe Lys Ile Tyr His Lys Cys Asp Asn
 485 490 495
 Ala Cys Ile Gly Ser Ile Arg Asn Gly Thr Tyr Asp His Asp Val Tyr
 500 505 510
 Arg Asp Glu Ala Leu Asn Asn Arg Phe Gln Ile Lys Gly Val Glu Leu
 515 520 525
 Lys Ser Gly Tyr Lys Asp Trp Ile Leu Trp Ile Ser Phe Ala Ile Ser
 530 535 540
 Cys Phe Leu Leu Cys Val Val Leu Leu Gly Phe Ile Met Trp Ala Cys
 545 550 555 560
 Gln Lys Gly Asn Ile Arg Cys Asn Ile Cys Ile
 565 570

- (2) INFORMATION FOR SEQ ID NO:22:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGGTTGGTCG CCGTTTCTAA CGCGATTCCC GGGGGTACC

39

- (2) INFORMATION FOR SEQ ID NO:23:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Trp Leu Val Ala Val Ser Asn Ala Ile Pro Gly Gly Thr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:24:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGGTTAGTCG CCGTGTCCTG CAGGCCAGAG AGGCCTTGGT ACC

43

- (2) INFORMATION FOR SEQ ID NO:25:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

RECTIFIED SHEET (RULE 91)
ISA/EP

GTCGCCGTGT CCAACGCG

18

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TAATTGGCCA GAGAGGCC

18

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGGGGATCCG GTACCAGCAA AAGCAGGGGA TAATTCTAT

39

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGGGGTACCC CCGGGGACTT TCCAGGAAAT GACAACAG

38

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCCGGTACCG AATCATCCTA GAAACAAGGG TGTTTTAAAT TAAT

44

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGGGAATTGC GTACCCCGG GAAGGCAATA ATTGTACTAC TCATGGT

47

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGTACCCCGG GGGATCGAAT CTGCACTGGG ATAACA

36

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGGGAATTCTG GATCCGGTAC CTCACAGACA GATGGARCAA GAAACATTGT

50

We claim:

1. A recombinant influenza HAO hemagglutinin protein expressed in a baculovirus expression system in cultured insect cells.
2. The protein of claim 1 further comprising a baculovirus signal peptide coupled directly to the HAO protein without intervening amino acids.
3. The protein of claim 1 further comprising a pharmaceutically acceptable carrier for administration as a vaccine.
4. The protein of claim 1 further comprising an adjuvant and a pharmaceutically acceptable carrier for administration as a vaccine.
5. The protein of claim 3 wherein the pharmaceutically acceptable carrier is a polymeric delivery system.
6. The protein of claim 1 wherein the influenza is selected from the group consisting of influenza A strains and influenza B strains.
7. The protein of claim 6 where the influenza infects humans.
8. The protein of claim 1 further comprising a second protein which is fused to the hemagglutinin.
9. The protein of claim 8 selected from the group consisting of hepatitis B viral proteins, HIV proteins, carcinoembryonic antigen, and neuraminidase.
10. A vector for making a recombinant influenza HAO hemagglutinin protein comprising the following 5' -> 3' sequences: a polyhedrin promoter from a baculovirus, an ATG translational start codon, a signal peptide, coding sequences for mature hemagglutinin from a strain of influenza, a translational termination codon, and a polyhedrin RNA polyadenylation signal.

11. The vector of claim 10 wherein the signal peptide is a baculovirus protein having a molecular weight of approximately of 61K and the amino acid sequence set forth in the first 18 amino acids of Sequence Listing ID No. 7.

12. The vector of claim 10 wherein the signal peptide is an influenza hemagglutinin protein promoter.

13. The vector of claim 10 wherein the sequence encoding the signal peptide and the hemagglutinin does not code for any intervening amino acids.

14. The vector of claim 10 further comprising sequence encoding a second protein which is expressed as a fusion protein with the hemagglutinin.

15. The vector of claim 10 transfected into cultured insect cells.

16. A method for making a recombinant influenza hemagglutinin protein comprising infecting cultured insect cells with a vector containing the following 5'→3' sequences: a polyhedrin promoter from a baculovirus, an ATG translational start codon, a signal peptide, the coding sequences for hemagglutinin from a strain of influenza selected from the group consisting of influenza A strains and influenza B strains, a translational termination codon, and a polyhedrin RNA polyadenylation signal, and culturing the cells in a nutrient media.

17. The method of claim 16 further comprising isolating the HAO influenza hemagglutinin protein from cells to a purity of at least 95%.

18. The method of claim 17 wherein the protein is isolated by separating the hemagglutinin from non-membrane proteins at an alkaline pH,

washing the membrane-bound proteins to elute the hemagglutinin, separating the hemagglutinin from other proteins binding to an anion exchange resin by a change in pH, and separating the hemagglutinin from other proteins binding to a cation exchange resin by a change in salt concentration.

19. A method for making a vector containing the following 5'→3' sequences: a polyhedrin promoter from a baculovirus, an ATG translational start codon, a signal peptide, the coding sequences for hemagglutinin from a strain of influenza selected from the group consisting of influenza A strains and influenza B strains, a translational termination codon, and a polyhedrin RNA polyadenylation signal comprising

harvesting virus from the cell media and isolating either viral RNA, for Influenza A strains, or mRNA, for Influenza B strains;

synthesizing cDNA using either an universal primer (5'-AGCAAAAGCAGG-3' (SEQ ID NO. 1)) for the viral RNA from the Influenza A strains or random primers for the mRNA from Influenza B strains, wherein the 5' and 3' primers have restriction enzyme sites at the ends that are not found within the hemagglutinin genes;

amplifying the influenza A or B primers and influenza cDNA mixed with the hemagglutinin gene segments to produce double-stranded DNA fragments containing entire mature hemagglutinin coding sequences;

identifying the signal peptide of the hemagglutinin genes then amplifying the hemagglutinin genes minus the signal peptide; and

cloning the hemagglutinin genes minus the signal peptide into a vector containing the AcNPV polyhedrin promoter.

20. The method of claim 19 wherein the hemagglutinin genes are cloned into the vector using PCR so that the vector encodes the signal peptide coupled directly to the hemagglutinin without any intervening amino acids.

21. The method of claim 19 further comprising transfecting the vector into insect cells, and selecting cells for hemagglutinin expression.

22. A method for vaccinating an animal against influenza comprising administering to the animal an effective amount of a recombinant influenza HAO hemagglutinin protein expressed in a baculovirus expression system in cultured insect cells.

23. The method of claim 22 further comprising administering the protein in a polymeric delivery system.

24. The method of claim 22 wherein the influenza is selected from the group consisting of influenza A strains and influenza B strains.

25. The method of claim 22 wherein the animal is selected from the group consisting of a mammal and an avian species.

26. The method of claim 22 wherein the animal is a human.

1/5

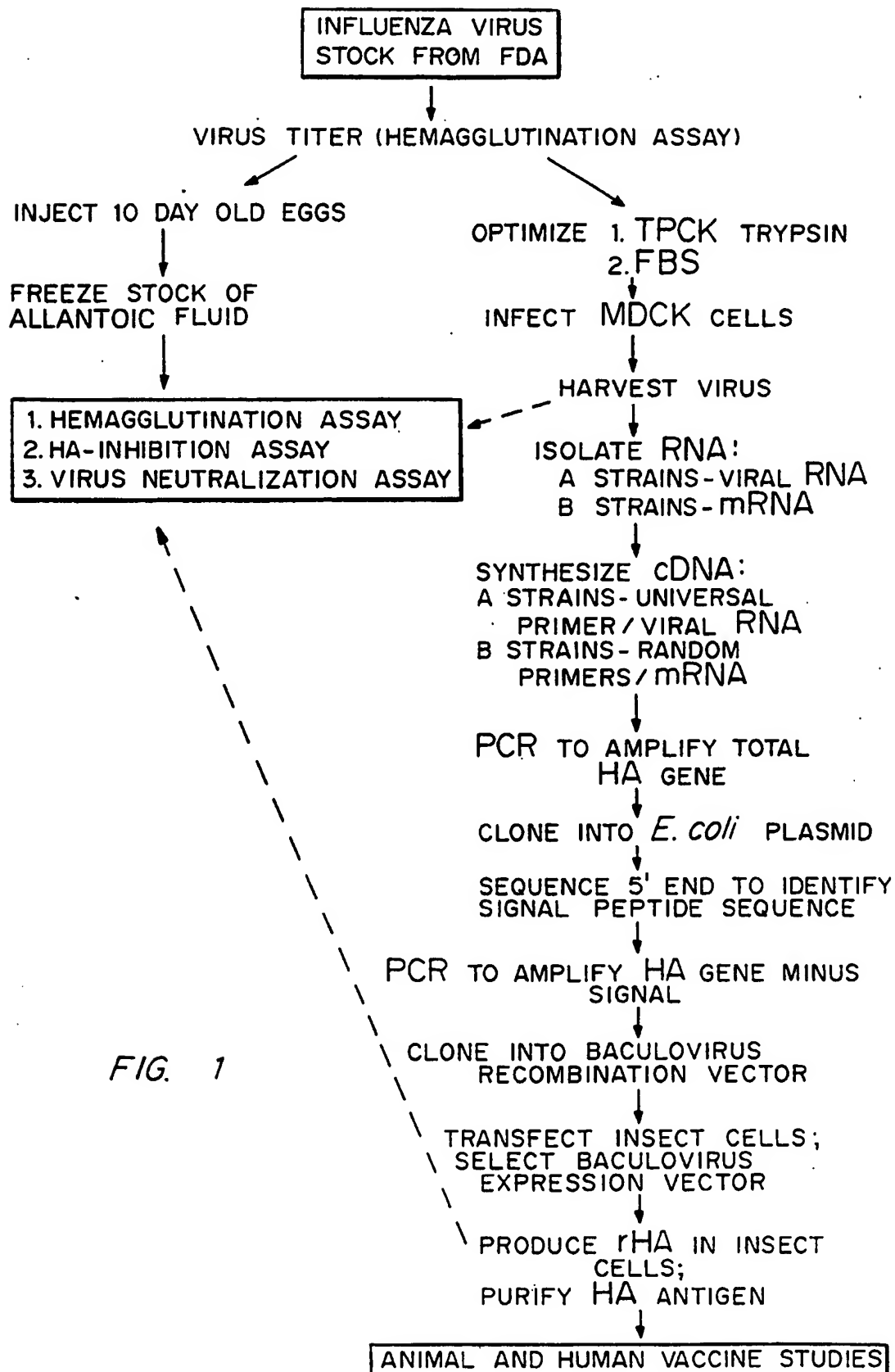


FIG. 1

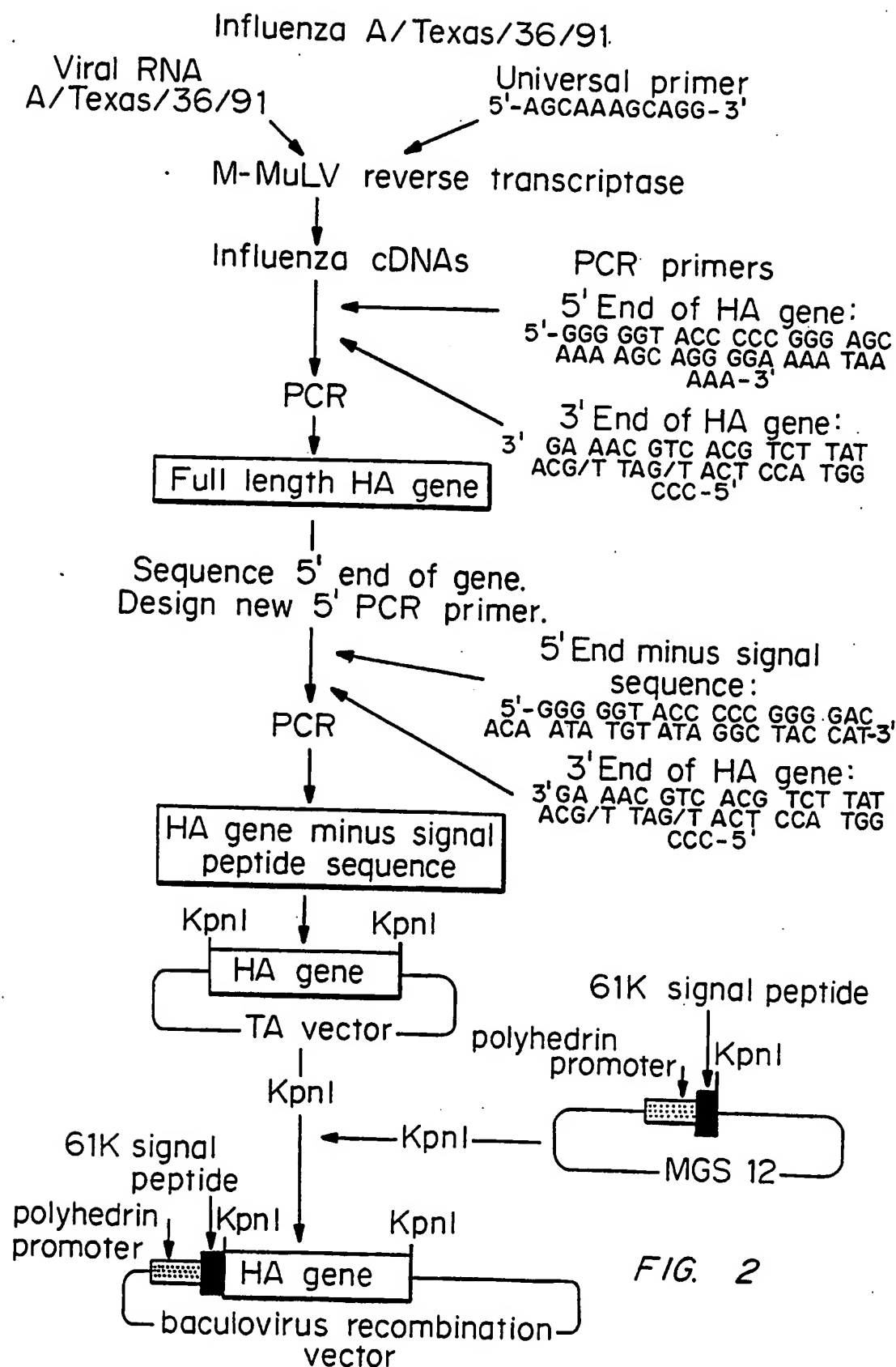


FIG. 2

3/5

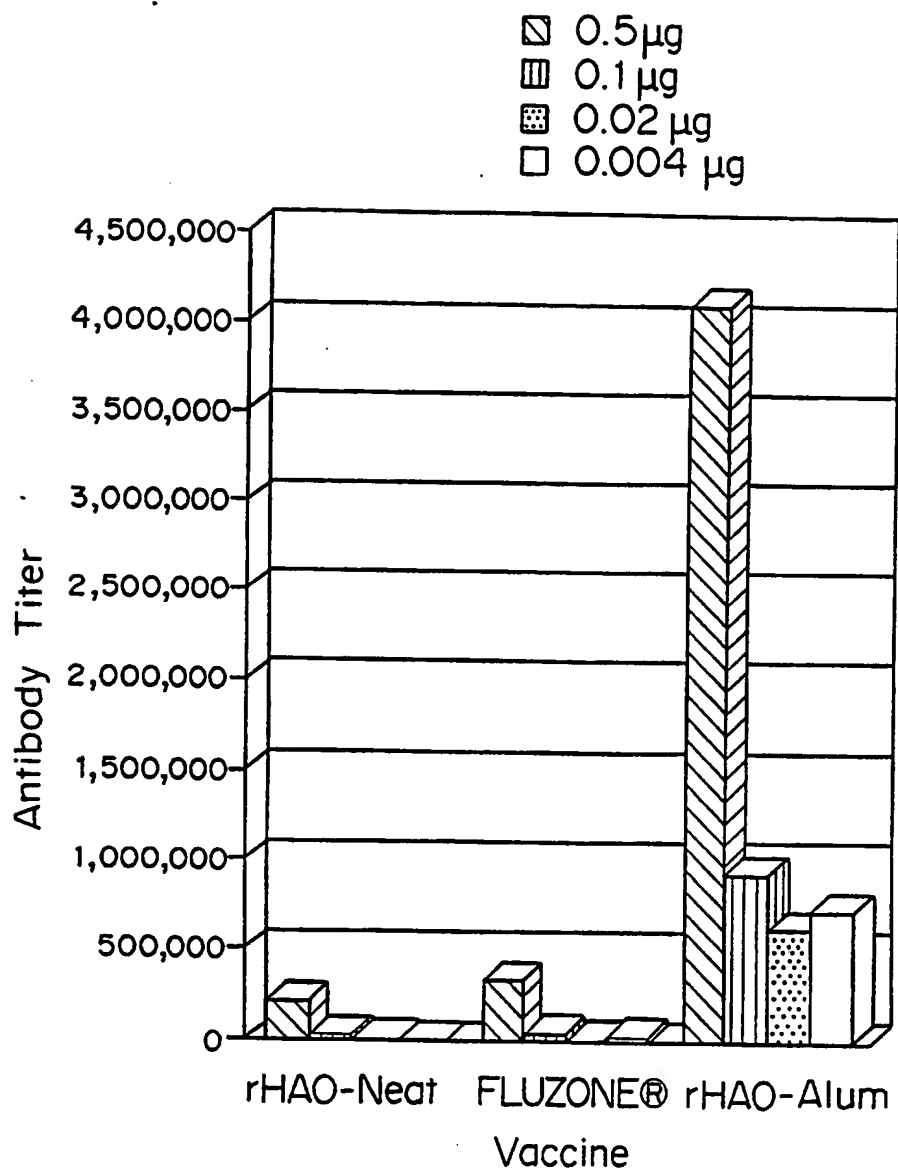


FIG. 3

4/5

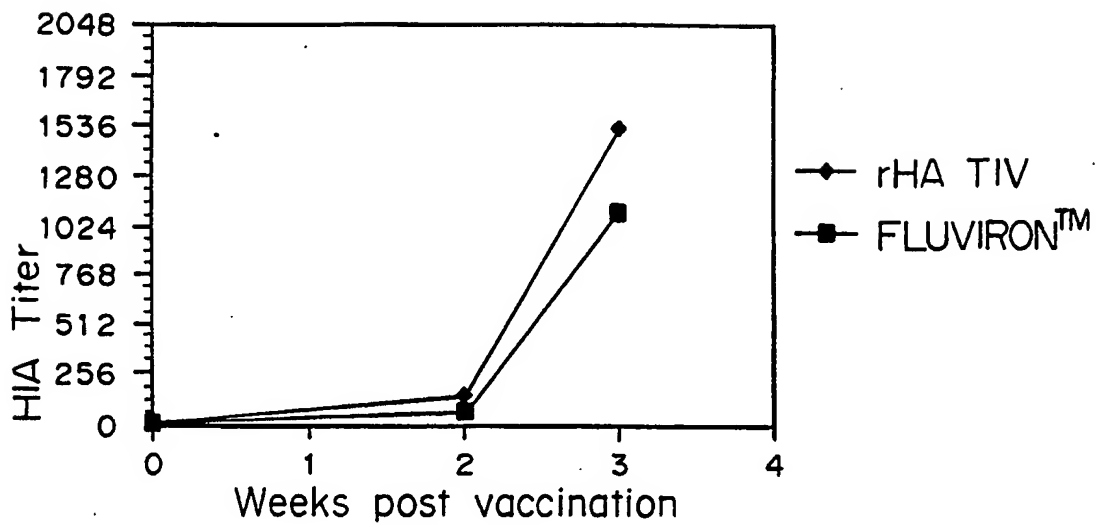


FIG. 4a

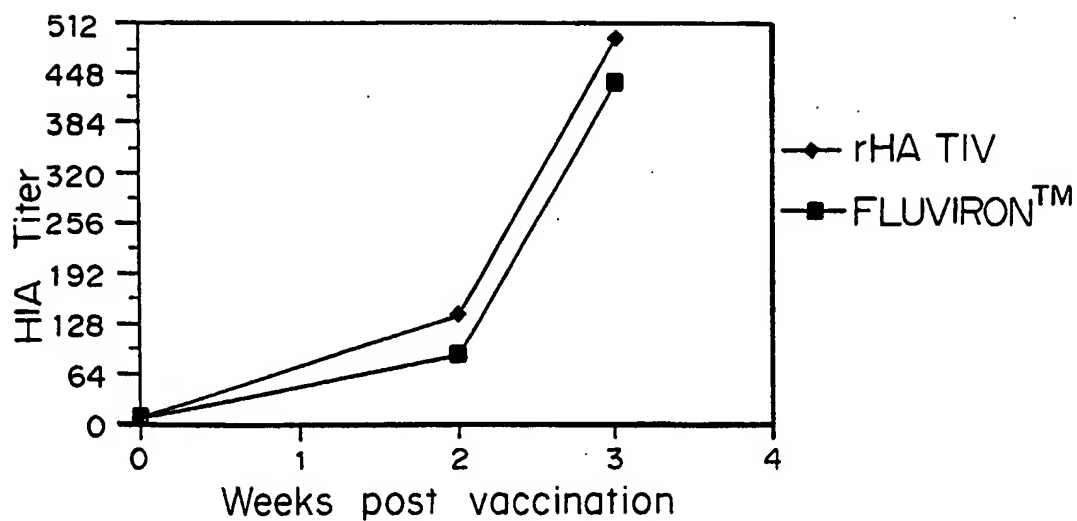


FIG. 4b

5/5

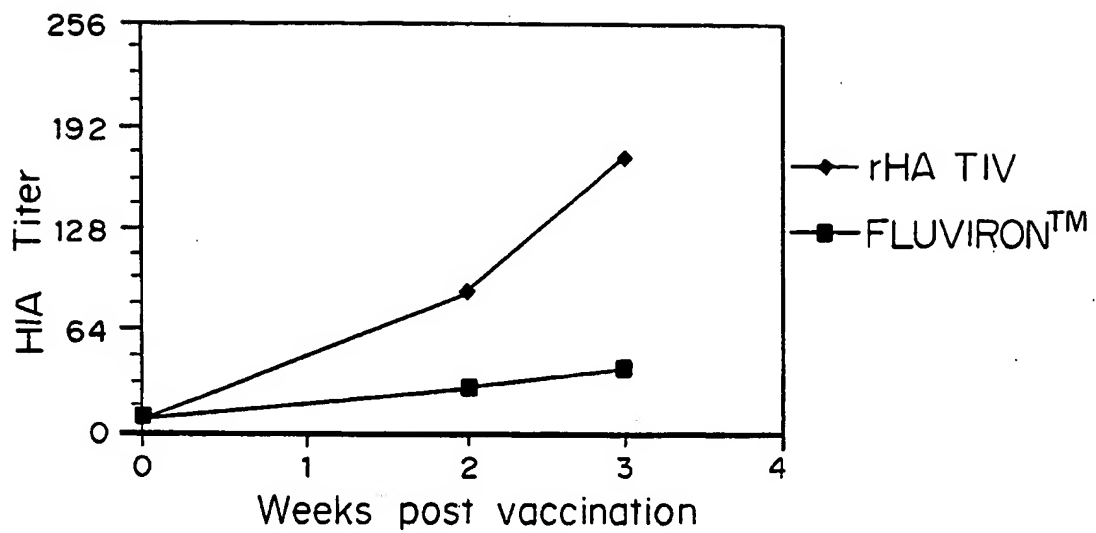


FIG. 4c

INTERNATIONAL SEARCH REPORT

Internat. Application No
PCT/US 95/06750

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/86 C12N15/62 C07K14/11 A61K39/145

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N C07K A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EMBO J., vol. 5, no. 6, June 1986 OXFORD UNIVERSITY PRESS,GB;, pages 1359-1365, K. KURODA ET AL. 'Expression of the influenza virus haemagglutinin in insect cells by a baculovirus vector'	1,2,10, 13,15
Y	see page 1359, right column, line 36 - line 45	14,16
X	--- VIRUS RES. (1986), 5(1), 43-59 CODEN: VIREF;ISSN: 0168-1702, July 1986	1
Y	POSSEE, R. D. 'Cell-surface expression of influenza virus hemagglutinin in insect cells using a baculovirus vector' see the whole document	6-8,10, 13-16
	--- -/-	

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
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- *O* document referring to an oral disclosure, use, exhibition or other means
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- *&* document member of the same patent family

Date of the actual completion of the international search

1 February 1996

Date of mailing of the international search report

20.02.96

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Fax (+31-70) 340-3016

Authorized officer

Hornig, H

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 95/06750

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
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Y	see page 1238, line 10 - page 1239, line 4 ---	6,7,10, 13-16
X	BIOTECHNOLOGY, vol. 6, no. 1, January 1988 NATURE PUBL. CO.,NEW YORK, US, pages 47-55, V.A. LUCKOW AND M.D. SUMMERS 'Trends in the development of baculovirus expression vectors' see table 1 ---	1,6 10,13-16
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Y	EP,A,0 546 787 (AMERICAN HOME PROD) 16 June 1993 see the whole document ---	1,6-10, 13-16
Y	WO,A,88 07082 (AMERICAN BIOGENETIC SCIENCES) 22 September 1988 see page 106, line 15 - page 119, line 7; claims 1-51 ---	1,6-10, 13-16
A	US,A,4 659 669 (KLEID ET AL.) 21 April 1987 see the whole document ---	1-26
A	VIROLOGY (1994), 202(2), 586-605 CODEN: VIRLAX;ISSN: 0042-6822, 1 August 1994 AYRES, MARTIN D. ET AL 'The complete DNA sequence of Autographa californica nuclear polyhedrosis virus' see the whole document ---	1-26
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INTERNATIONAL SEARCH REPORT

Intern : Application No
PCT/US 95/06750

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
T	<p>VIROLOGY (1995), 212(2), 673-85 CODEN: VIRLAX; ISSN: 0042-6822, 1 October 1995 HAWTIN, RACHAEL E. ET AL 'Identification and preliminary characterization of a chitinase gene in the Autographa californica nuclear polyhedrosis virus genome' see the whole document ---</p>	1-26
T	<p>JOURNAL OF INFECTIOUS DISEASES 171 (6). 1995. 1595-1599. ISSN: 0022-1899, June 1995 POWERS D C ET AL 'Influenza A virus vaccines containing purified recombinant H3 hemagglutinin are well tolerated and induce protective immune responses in healthy adults.' see the whole document ---</p>	1-26
T	<p>WO,A,95 32286 (MICROGENESYS INC) 30 November 1995 see page 18, line 33 - page 20, line 9 -----</p>	10,11

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Information on patent family members

International Application No

PCT/US 95/06750

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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		AU-B- 1542488	10-10-88
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		EP-A- 0349583	10-01-90
		JP-T- 2502873	13-09-90
		WO-A- 8807087	22-09-88
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US-A-4659669	21-04-87	NONE	
WO-A-9532286	30-11-95	NONE	